Toxicity

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BIOMARKERS OF EXPOSURE TO TOXIC SUBSTANCES

Volume II: Genomics:
Unique Patterns of Differential Gene Expression and Pathway Perturbation Resulting from Exposure to Nephrotoxins with Regional Specific Toxicity

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14. ABSTRACT

Toxicity commonly occurs after exposure to a variety of chemicals agents. Changes in gene expression are among the most sensitive indicators of chemical exposure. Toxicogenomics, which is based on DNA microarray technology, is the study of the cellular response to chemical insults at the transcriptomic level by simultaneous measurement of the expression levels of virtually all expressed genes. Therefore, this technology is a useful technique for studying the molecular mechanism of chemical-induced toxicity. In this study, DNA microarray technology was used in combination with advanced bioinformatic techniques to evalauate its utility in assessing gene expression changes and subsequently the mechanism of renal injury following exposure to nephrotoxins selected for their regional specific toxicity. Four chemicals, hippuric acid, D-serine, puromycin and amphotericin B, which induce glomerular and tubulointerstitial damage, necrosis of the pars recta region of the proximal tubules, glomerular injury, and distal tubular damage, respectively, were used in this study. The effects of exposure to these chemicals on renal differential gene expression and the biological implication of these gene expression changes were investigated.

15. SUBJECT TERMS

Amphotericin B, bioinformatics, cell cycle regulation, clinical, clustering analysis, D-serine, glomerular injury, hippuric acid, histopathologic analysis, microarray, pathway analysis, proximal tubular damage, puromycin, renal injury, transcription regulation

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FORWARD

This research program is documented in a final technical report comprised of five volumes. Volume I provides a global overview of the entire effort. Volumes II-IV provide the technical details of the three approaches (genomics, proteomics, and metabonomics) used to identify the relevant biomarkers of toxic effects. Volume V describes the effort to perform pre-validation of the identified biomarkers. Figure 1 shows this technical report structure.

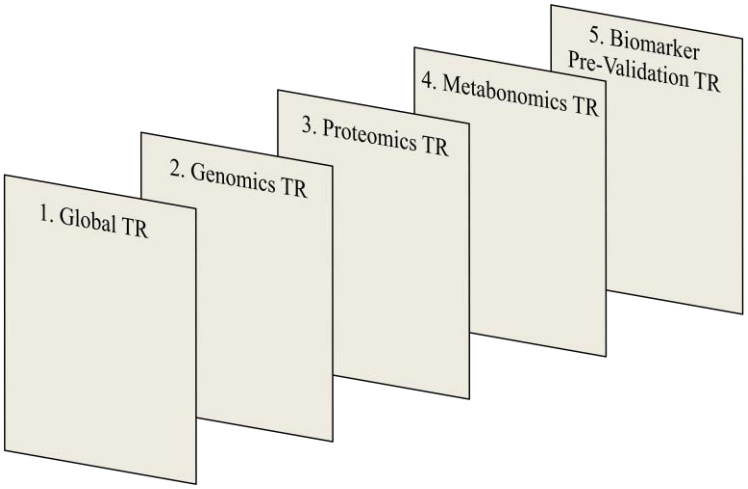

Figure 1: Technical Report Volume Order

Volume one contains the experimental design, explains how the needs of the warfighter led to conducting this research effort, the reasoning behind the specific analysis method and biomarker selections, and the manner in which the specimens were collected. The sample analysis is captured in the second, third, and fourth reports (Genomics, Proteomics, and Metabonomics). The three analytical and investigational approaches were conducted in parallel and fed data into the fifth report (Biomarker Pre-validation) as depicted in Figure 2.

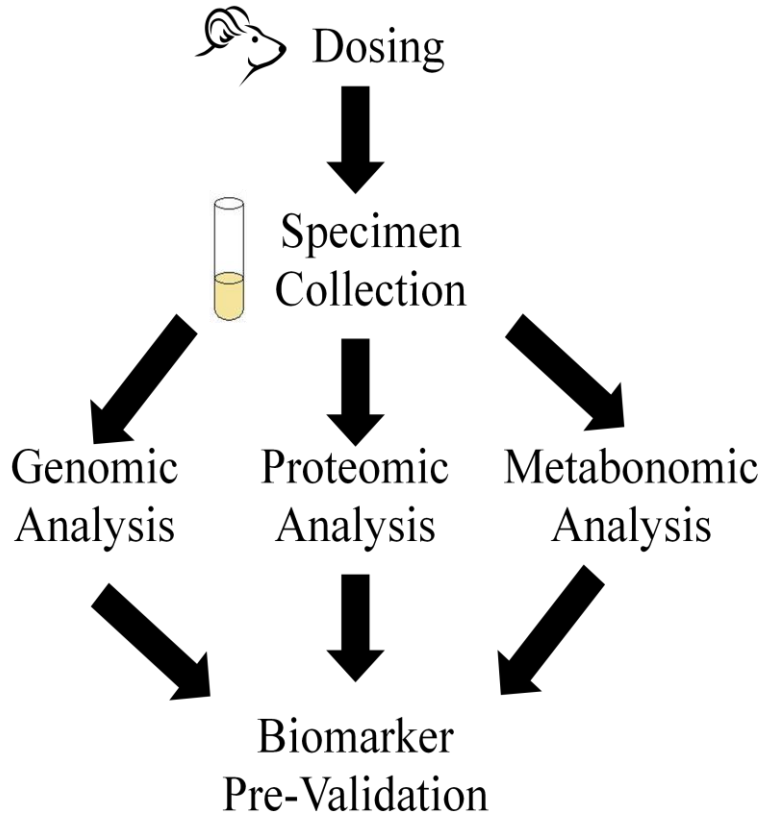

Figure 2: Work Unit Investigational Overview

Over 80 Department of Defense civilians, contractors, and military contributed in the research spanning five years.

PREFACE

This research was accomplished at the Applied Biotechnology Branch, Human Effectiveness Directorate of the 711th Human Performance Wing (711 HPW/RHPB) of the Air Force Research Laboratory, Wright-Patterson AFB, OH, under Dr. John J. Schlager, Branch Chief. This technical report was written for AFRL Work Unit 7184D405.

All studies involving animals were approved by the Wright-Patterson Institutional Animal Care and Use Committee, and were conducted in a facility accredited by the Association for the Assessment and Accreditation of Laboratory Animal Care, International, in accordance with the *Guide for the Care and Use of Laboratory Animals* (1996).

SUMMARY

In this study, the use of DNA microarray technology combined with advanced bioinformatic techniques was evalauated for its utility in assessing the molecular mechanisms of renal injury following exposure to four nephrotoxins including hippuric acid (HPA), D-serine, puromycin (PUR) and amphotericin B (AMPB), which induce glomerular and tubulointerstitial damage, necrosis of the pars recta region of the proximal tubules, glomerular injury, and distal tubular damage, respectively. Using a stringent approach, where only differential expression of the genes commonly identifed by at least two statistical methods (with correction for multiple testing) were considered statistically significant, exposure to HPA, D-serine, and PUR resulted in renal differential expression of 206, 1907, and 1127 genes, respectively. However, there were no significant gene expression changes in the kidney after AMPB treatment. Although the reason for this is not completely clear, this is likely due to the formation of AMPB deposits on the outside of the kidney, as noted in the histopathologic analysis. The biological implications of differential gene expression induced by HPA, D-serine, and PUR exposure were subsequently investigated using advanced bioinformatics including gene ontology analysis and pathway analysis. Coupled with Self Organizing Map (SOM) clustering analysis, co-regulated gene clusters with unique dose responses were identified. Gene ontology and pathway analyses revealed that these gene clusters were involved in specific biological processes/pathways correlating with phenotypic changes as indicated in the clinical chemistry and histopathology analyses. For instance, cellular pathways such as cell cycle regulation, mitotic sister chromatid segregation, transcription regulation, and mRNA metabolism, processing, splicing and transport were preferentially affected by HPA treatment. On the other hand, D-serine treatment appeared to up-regulate pathways including actin cytoskeleton biogenesis and organization, apoptosis, cell adhesion, cell cycle regulation, DNA repair, DNA replication and packaging and chromatin assembly, protein metabolism and transport, inflammatory response, proteasome-mediated protein degradation, Ras and TGF-beta signaling pathways, protein synthesis, and mRNA transcription, processing, splicing and transport. Conversely, major cellular metabolic pathways including carbohydrate, amino acid, lipid, nucleotide, vitamin and energy metabolisms seemed to be down-regulated after D-serine exposure. Similarly, a large number of biological processes and pathways were affected after PUR treatment including down-regulation of cellular metabolic pathways (e.g. metabolisms of amino acid, lipid, carbohydrate metabolism, nucleotide, coenzyme, cofactor, hormone, and energy production), cellular response to steroid hormones, insulin, and xenobiotics, and up-regulation of pathways regulating cellular morphogenesis, actin cytoskeleton organization and biogenesis, acute inflammatory/immune response, wound healing and tissue remodeling, angiogenesis, cell growth and death, chromosome biogenesis and organization, protein synthesis, ubiquitin proteasome-mediated protein degradation, and RNA transcription, processing, splicing and transport. In addition, biological association network analysis was performed and the results provided novel insights into the functional interactions of the differentially expressed genes with their potential partners of diverse nature such as gene promoters, proteins and small molecules. Interestingly, these chemical treatments, with the exception of AMPB, resulted in chemical-specific patterns of differential gene expression and pathway perturbation. Collectively, the combined results of these bioinformatic analyses provided important insights into the molecular basis for the perturbation of cellular processes and pathways that will facilitate further understanding of the coordination of the cellular response to these toxic insults. To fully understand the molecular mechanisms of the cellular response to the

exposure of these compounds, detailed analysis of the temporal response of the transcriptomic profile to a broad dose range might be needed. Such analysis would likely allow the delineation of adaptive response, as well as toxic response that ultimately leads to nephrotoxin-induced organ damage. As demonstrated in this study, a combined use of advanced biotechnologies, such as DNA microarrays and bioinformatics, allows the identification of the molecular mechanisms of nephrotoxin-induced renal differential gene expression, which will ultimately facilitate the identification of mechanism-based biomarkers for chemical exposure or other environmental stressors. If a large number of data sets consisting of chemicals with diverse target organ specificity were available, differential gene expression identified using an approach similar to that employed in this study could potentially become useful biomarkers for early detection and/or prediction of organ damage. However, it should be emphasized that in analyzing DNA microarray data, the biological relevance of gene expression changes response to perturbations has to be evaluated in the context of phenotypic changes: adaptive response, toxic response, repair, apoptosis/necrosis, or regeneration. For example, induction of genes associated with DNA repair represents an essential defense mechanism of the organism, but may also be an indication of the occurrence of DNA damage. If the damage is extensive, other pathways such as apoptosis may be activated to eliminate the damaged cell population that is beyond repair. A global view of changes in cellular pathways as provided by pathway analysis of the DNA microarray data will facilitate the proper interpretation of the significance of these changes, which in turn will facilitate the assessment of cellular integrity, as well as disturbance of homeostasis of all the levels of cells, tissues and organs. Ultimately, this information will guide subsequent studies investigating changes in protein contents (and activities) as biomarkers for chemical exposure.

1. INTRODUCTION

Toxicity commonly occurs after exposure to a variety of chemical agents. Changes in gene expression are among the most sensitive indicators of chemical exposure. Toxicogenomics, which is based on DNA microarray technology, is the study of the cellular response to chemical insults at the transcriptomic level by simultaneous measurement of the expression levels of virtually all expressed genes. Because of its global coverage, DNA microarray technology is useful for studying the molecular mechanism of chemical-induced toxicity. In this study, we used DNA microarray analysis combined with advanced bioinformatic techniques to evalauate its utility in assessing gene expression changes and subsequently the mechanism of renal injury following exposure to nephrotoxins selected for their regional specific toxicity. Four chemicals, hippuric acid, D-serine, puromycin and amphotericin B, which induce glomerular and tubulointerstitial damage, necrosis of the pars recta region of the proximal tubules, glomerular injury, and distal tubular damage, respectively, were used in this study. The effects of exposure to these chemicals on renal differential gene expression and the biological implication of these gene expression changes were investigated.

2. METHODS AND MATERIALS

2.1. Animal Treatment and Tissue Collection

Male rats F-344 were randomly assigned to groups of three to five animals and each group was dosed intraperitoneally with one of the following concentrations, hippuric acid (HPA - 0, 5, 50, 500, 750, 1,000, and 1,250 mg/kg), D-serine (0, 5, 20, 50, 200, and 500 mg/kg), puromycin (PUR - 0, 5, 25, 75 and 150 mg/kg), amphotericin B (AMPB - 0, 1, 5, 10, 50, and 50 mg/kg). Control and treated animals were sacrificed by inhalation of carbon dioxide at 4 days (HPA and D-serine) or 7 days (PUR and AMPB) after dosing. Tissue samples of kidneys were collected from control and nephrotoxin-treated animals. Specifically, the transverse region of the right kidney weighing ~30 mg were prepared from the animals, immediately frozen in liquid nitrogen and stored at -80^{o}C until processed for total RNA isolation. The remaining kidney tissues were fixed in 10% neutral-buffered formalin, routinely processed and embedded in paraffin blocks. Histological sections in five-micrometer thickness were prepared, mounted on glass slides, and stained with hematoxylin and eosin (HE).

2.2. Serum Chemistry

Blood samples via portal vein were collected in sodium heparin tubes (Becton-Dickinson) and sera were recovered by centrifugation at 1,100 x g at 25^{o}C for 10 min. Typical biochemical markers for hepatotoxicity, such as alkaline phosphatase [ALKP], alanine aminotransferase [ALT], aspartate aminotransferase [AST] and total bilirubin [TBIL], were measured using an IDEXX Vet Test 8008 Clinical Chemistry Analyzer. Similarly, serum chemistry for selected markers of renal dysfunctions, including total bilirubin [TBIL], creatinine [CREA], urea nitrogen [BUN], and total protein [TP], were also analyzed.

2.3. RNA Isolation

Total RNA was isolated from one piece of kidney tissue weighing ~30 mg from treated or control animals using Qiagen RNeasy Mini Kit (Qiagen, Valencia, CA). Frozen tissues were homogenized in lysis buffer containing guanidinium thiocyanate and β-mercaptoethanol. Extraction and purification of total RNA from tissue homogenates were performed according to the manufacturer's instructions. The quality of the isolated RNAs was confirmed using the RNA 6000 Nano LabChip Kit with the Agilent 2100 Bioanalyzer System (Agilent Biotechnologies, Palo Alto, CA). Concentration of total RNA was determined using the NanoDrop 1000 spectrophotometer (NanoDrop Technologies, Wilmington, DE). Samples with a concentration lower than 0.125 µg (microgram) total RNA per µl (microliter) were concentrated using Microcon Centrifugal filters.

2.4. Target Preparation and GeneChip Hybridization/Scanning

Fifteen micrograms of total RNA was used for the first strand cDNA synthesis followed by the second strand synthesis using the SuperScript Choice system (Invitrogen Corporation, Carlsbad, CA) in the presence of an oligo-(dT)24 anchored T7 primer (Proligo, Boulder, CO). The resulting cDNA was used as the template for *in vitro* transcription using the BioArray High Yield RNA Transcript Labeling Kit (Enzo Diagnostics, Inc., Farmingdale, NY). The concentration and purity of each cRNA sample were then determined by measuring the A_{260}/A_{280} ratio. Twenty micrograms of each biotin-labeled cRNA sample was fragmented using 5X Affymetrix Fragmentation Buffer. Hybridization cocktail containing 15 µg fragmented cRNA, Affymetrix Control Oligo B2, Affymetrix Eukaryotic Hybridization Control, Herring Sperm DNA, Acetylated BSA, 1X Hybridization Buffer (final concentration), DMSO, and RNase-free water was heated to 99°C for 5 min, then incubated at 45°C for 5 min before being loaded onto an Affymetrix Rat Genome RAE230A GeneChip array. Hybridization was performed at 45°C for 16 h in an Affymetrix hybridization oven with constant end over end rotation at 60 RPM. Once hybridization was complete, the hybridization mix was removed from each GeneChip, and the microarrays were washed in the Affymetrix GeneChip Fluidics Station 450 using a non-stringent wash buffer at 25°C followed by a stringent wash buffer at 50°C. After washing and staining, the GeneChips were scanned in the Affymetrix GeneChip Scanner 3000 using the Affymetrix GeneChip Operating Software (GCOS, version 1.2). The fluorescence intensity was captured and stored as .DAT files in the Affymetrix GCOS software according to standard Affymetrix procedures.

2.5. Data Analysis and Biological Interpretation

Absolute gene expression was determined using the Affymetrix GCOS Statistical Algorithm. This algorithm provides a single expression level for each gene based on the fluorescence intensity of the probe set representing each gene, i.e., 11 Perfect Match (PM) and 11 Mismatch (MM) paired probes. The MM probes act as specificity controls that allow for direct subtraction of background and/or cross-hybridization signals. This algorithm also provides a qualitative measure for the signal referred to as "detection p-value," which can be used to divide the genes into three groups, "Present" (P), "Marginal" (M), or "Absent" (A),

respectively. To facilitate inter-experimental comparison, the gene expression signal was scaled using "All Probe Sets Scaling" with a target intensity of 500. The processed GeneChip data (.CHP file) was then published into a GCOS Publish Database for data analysis and data export.

Identification of differential gene expression was performed using the t-test analysis module of the Affymetrix Data Mining Tool (DMT), ANOVA and SAM (Significant Analysis of Microarrays) modules of the TIGR MultiExperiment Viewer (TMeV) (from Genomic Research Institute). The differentially expressed genes identified in each dose of the chemical treatments were compared. To increase the stringency of the analysis, only the genes with $p<0.01$ over two consecutive doses were considered as differentially expressed. In addition, differential gene expression was also determined using the ANOVA ($p<0.01$, with adjusted Bonferonni correction) and the SAM (with S0 selection by method of Tusher et al., 2001 and no Q-value calculation) modules of the TmeV software (version 4.0). Only the genes that were identified in at least two of three analyses were included in the final list of differentially expressed genes.

To group the genes with similar dose response in terms of gene expression changes to chemical treatment, Hierarchical Clustering Analysis (HCA) using the TIGR MultiExperiment Viewer (TMeV) (from Genomic Research Institute) or Self Organizing Map (SOM) clustering analysis was performed using DMT with the expression profiles of the differentially expressed genes as input data. In addition, the gene expression dataset was exported to Excel or text files for pathway analysis and biological interpretation.

To identify gene ontology categories and pathways significantly enriched (i.e., over-represented) among the differentially expressed genes, the entire list of differentially expressed genes, as well as the lists of up- and down-regulated genes were used as input data to search the databases in the DAVID (Database for Annotation, Visualization, and Integrated Discovery) website (Dennis et al., 2003). To visualize the involvement of the differentially expressed genes in specific biological pathways, pathway analysis was performed using GenMAPP (Gene MicroArray Pathway Profiler, version 2.1, Gladstone Institute, University of California at San Francisco, San Francisco, CA). Biological association networks of the differentially expressed genes were also constructed using PathwayArchitect, version 2.0.1 (Stratagene, La Jolla, CA), a tool that is based on the mining of the open literature, network modeling, and relevance statistics to map gene/protein associations and infer biological and functional interactions. Filters for cellular functions such as transcription regulation, protein binding, transport regulation, etc. were applied to construct biological association networks for these specific functions. The resulting biological association network maps without further pruning were used for empirical exploration of their biological implications.

3. RESULTS

3.1. Histopathologic Analysis

Frozen sections of the kidney were evaluated for necrosis and graded on a 1-4 scale (1 being minimal and 4 being marked or severe) on eight morphological features: tubular eosinophilic fluid, mineral corpora amylacea, nephropathy, mixed inflammation, suppurative inflammation, pyelonephritis, dilated lymphatic leukocytosis, and papillary necrosis.

3.1.1. Hippuric acid (HPA) Treatment

No histological lesions in the kidney could be definitively attributed to HPA administration (data not shown). The presence of mineral (corpora amylacea) within renal tubules was noted in some control and HPA-treated animals. Since this is a common background lesion in the kidney of rats, it was therefore considered to be unrelated to HPA treatment. Marked suppurative inflammation with bacterial colonies was observed in multiple tissues of one animal (1000 mg/kg) and appeared to be due to complications from improper venous catheter placement into the right atrium resulting in a showering of thrombotic emboli.

3.1.2. D-Serine Treatment

The results of histopathologic analysis of the kidney samples 96 hr after D-serine treatment are shown in Table 1. Progression of renal tubular alterations (nephropathy) with moderate to significant severe histopathological scores was observed in the kidney tissues from all animals exposed to 200 and 500 mg/kg D-serine. Specific changes included cortical and medullary tubular ectasia, attenuation and regeneration of tubular epithelial cells, thickening of tubular basement membranes, and intratubular eosinophilic protein fluid. However, no significant effects were observed at these two doses with respect to other kidney histopathologic endpoints. Despite that one animal from each of the three dose groups of 5, 200 and 500 mg/kg showed signs of pyelonephritis, the overall effects of D-serine exposure up to 50 mg/kg did not produce any histopathologic findings in the kidney. Control animals and animals exposed up to 50 mg/kg D-serine exhibited mild severity with respect to kidney mineral corpora amylacea. As discussed above, this was considered unrelated to the D-serine exposure.

Table 1: Histopathology Analysis of the Kidney Tissues for the Control and Treated Animals 96 Hours after D-Serine Exposure

Dose (mg/kg)	Control					5					20					50					200					500				
Animal #	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5
Tubular eosinophilic fluid	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	3	3	3	3	3	3	3
Mineral corpora amylacea	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
Nephropathy	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3	3	3	3	3	3	3	3	3
Inflammation, mixed	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Inflammation, suppurative	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pyelonephritis	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	2	0
Dilated lymphatics leukocytosis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

0 = No abnormal findings; 1 = Minimal; 2 = Mild; 3 = Moderate; 4 = Marked/Severe

= Significantly different from Control (P < 0.008); paired comparisons between the dosed and the control groups were performed using Mann-Whitney Rank Sum Test.

3.1.3. Puromycin (PUR) Treatment

Histopathologic analysis of the kidney tissues obtained on day 7 after PUR treatment revealed mild lesions in the animals dosed with 150 mg/kg of PUR. Histological changes included multifocal mild dilation of kidney tubules that were occasionally lined by attenuated or flattened tubule epithelial cells. Mitotic figures that were present in cells lining these tubules likely represented regeneration of damaged tubule epithelial cells (Table 2). Protein casts present in some tubules were characterized by eosinophilic, hyaline material filling tubular lumens. However, there was no evidence of damage to the glomerular podocytes as observed by light microscopy.

Table 2: Histopathology Analysis of the Kidney Tissues for the Control and Treated Animals 168 Hours after PUR Exposure

Dose (mg/kg)	Control				5					25					75					150				
Animal #	1	2	3	4	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5	1	2	3	4	5
Tubular Cell Degeneration	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tubular Cell Eosinophilic Droplets	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1
Mineral Corpora Amylacea	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Nephropathy	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	2	2
Inflammation, mixed	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Inflammation, suppurative	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Pyelonephritis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Tubular Cast Formation	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Dilated Lymphatics, Leukocytosis	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

0 = No abnormal findings; 1 = Minimal; 2 = Mild; 3 = Moderate; 4 = Marked/Severe

= significantly different ($p < 0.0001$); paired comparisons between the dosed and the control groups were performed using Mann-Whitney Rank Sum Test.

3.1.4. Amphotericin B (AMPB) Treatment

Results of histopathologic analysis of the kidney samples from the AMPB study were inconclusive, since there were deposits of AMPB on the outside of the organs. It was thus decided that no additional analyses should be performed.

3.2. Clinical Chemistry

Blood samples were collected from control and treated animals at 24 and 96 (or 168) hr after treatment. Plasma levels of total bilirubin (TBIL), creatinine (CREA), urea nitrogen (BUN) and total protein (TP) were measured to assess treatment-related nephrotoxicity.

3.2.1. HPA Treatment

There were no significant differences in the serum chemistry between control and HPA-treated animals on day 4 post-treatment (data not shown).

3.2.2. D-Serine Treatment

The results of clinical chemistry analysis indicated that only rats in the 200 and 500 mg/kg dose groups showed a significant decrease in TBIL 24 hr following exposure compared to the control group, while the levels of CREA and BUN were significantly increased (Table 3). However, no significant change in TBIL was observed in any dose groups at the termination of the study (96 hr post-dosing). The CREA level in the rats dosed with 200 mg/kg D-serine returned to normal by 96 hr. In contrast, the level of BUN showed persistent elevation even at terminal sacrifice, although a small reduction compared to the 24 hr level was observed. On the other hand, rats exposed to 500 mg/kg D-serine exhibited elevated CREA and BUN that remained significantly increased throughout the entire course of the study (Table 3). In fact, animals in this dose group showed the highest BUN level at 96 hr post-treatment. No significant change in TP was observed in any dose group.

Table 3: Effect of D-Serine Treatment on Selected Serum Chemistry Parameters

Treatment (mg/kg)	TBIL (mg/dL)		CREA (mg/dL)		BUN (mg/dL)		TP (mg/dL)	
	24h	96h	24h	96h	24h	96h	24h	96h
0	5.5±1.3	1.6±0.8	0.3±0.1	0.5±0.1	15±1.6	17.8±1.9	6.1±0.1	6.7±0.3
5	5.4±2.9	1.9±0.8	0.4±0.1	0.4±0	13.8±2.4	18±1.2	5.9±0.3	6.7±0.2
20	4.1±0.2	2.2±1.1	0.4±0.1	0.4±0	16.3±1.5	16.8±1.8	6±0.2	6.7±0.2
50	5±1.4	1.2±1.2	0.4±0	0.4±0	15.3±1.3	16.2±1.9	6±0.3	6.5±0.3
200	*3.5±.7	1.5±0.7	*1.6±.3	0.7±0.2	*7.7±5.1	*7.8±14.2	6.2±0.3	6.7±0.3
500	*3.2±.5	1.7±0.4	*1.7±.2	*1.2±.2	*5.6±4.2	*6.5±3.4	5.8±0.3	7.1±0.4

Plasma from blood samples collected at 24 and 96h after DSER treatment were used in this analysis. Kidney enzymes include: total bilirubin (TBIL), creatinine (CREA), urea nitrogen (BUN), and total protein (TP).
**Significantly different than control ($p < 0.05$).*

3.2.3. PUR Treatment

Four of five animals treated with PUR at 300 mg/kg died within 24 hr, probably due to severe nephrotoxicity. The remaining animal from this dose group was not included in this study. Statistical analysis of the clinical chemistry results indicated that PUR treatment at 150 mg/kg failed to significantly alter the level of CREA, suggesting the absence of marked renal dysfunction (Table 4). Conversely, the levels of BUN in rats treated with 75 mg/kg were significantly increased compared with the low-dose treatment groups (i.e. 5 and 25 mg/kg) 24 hr after PUR exposure. One of the five rats treated with 150 mg/kg PUR showed persistent BUN elevation on day 7, in contrast to the fact that the BUN levels of other animals in the same group, as well as the animals treated with 75 mg/kg PUR, had returned to normal on day 7. TP levels

were significantly decreased in the 75 and 150 mg/kg treatment groups compared with the control and the low-dose groups 24 hr post-dosing, a finding that has been previously observed in PUR-induced nephrotic syndrome (Pedraza-Chaverrí et al., 1990; Pedraza-Chaverrí et al., 1993). While the TP level of the animals in the 75 mg/kg treatment group showed recovery on day 7, the animals dosed with 150 mg/kg of PUR showed a persistent decrease in the TP level.

Table 4: Effect of PUR Treatment on Selected Serum Chemistry Parameters

Treatment (mg/kg)	CREA (mg/dL)		BUN (mg/dL)		TP (g/dL)	
	24h	**168h**	**24h**	**168h**	**24h**	**168h**
0	0.4 ± 0.1	0.4 ± 0.1	13.5 ± 0.7	17.3 ± 1.9	7.3 ± 0.6	6.3 ± 0.1
5	0.3 ± 0.1	0.3 ± 0.0	14.6 ± 1.5	16.4 ± 1.9	6.9 ± 0.4	6.4 ± 0.2
25	0.4 ± 0.1	0.3 ± 0.0	13.0 ± 1.4	14.0 ± 1.4	6.7 ± 0.1	5.5 ± 0.1
75	0.4 ± 0.1	0.2 ± 0.1	18.4 ± 2.5[B]	15.0 ± 1.9	5.6 ± 0.4[AB]	5.9 ± 0.3
150	0.4 ± 0.0	0.2 ± 0.1	18.0 ± 1.8	21.0 ± 9.5	5.1 ± 0.1[AB]	4.5 ± 0.3[C]

Plasma from blood samples collected at 24 and 168h after PUR treatment were used in this analysis.
Kidney enzymes include: creatinine (CREA), urea nitrogen (BUN), and total protein (TP)
[A]*Significantly different than control ($p < 0.05$)*
[B]*Significantly different than 5 mg/kg & 25 mg/kg ($p < 0.05$)*
[C]*Significantly different than all doses ($p < 0.05$)*

3.2.4. AMPB Treatment

The results of clinical chemistry analyses of the samples from the AMPB study are shown in Table 5. While several results were significantly different from control groups, all values were well within their respective normal ranges.

Table 5: Effect of AMPB Treatment on Selected Serum Chemistry Parameters

Treatment (mg/kg)	TBIL (mg/dL)		CREA (mg/dL)		BUN (mg/dL)		TP (mg/dL)	
	24hr	168hr	24hr	168hr	24hr	168hr	24hr	168hr
0	7.6±4.5	6.7±1.6	0.3±0.1	0.2±0.1	14±1.2	14.2±1.1	5.5±0.4	6±0.2
1	8.8±5.2	3.4±1.9*	0.3±0.1	0.3±0.1	13±0.8	11.8±1.3*	5.8±0.2	5.6±0.3*
5	10.3±1.9	3±1.1*	0.4±0.1	0.1±0.1	13±1.2	12.8±1.3	5.5±0.1	5.8±0.2
10	6.9±4	6.6±2.5	0.3±0.1	0.1±0.1	13.5±0.6	12.8±1.8	5.3±0.3	6±0.3
25	2.3±1.2*	3.3±1.5*	0.3±0.1	0.1±0.1	14±1	12.6±0.5*	5.8±0.6	5.9±0.1
50	7.7±2.2	5.1±2.3	0.3±0	0.3±0.1	12.6±1.1	14.2±1.6	5.4±0.4	6.1±0.2

Plasma from blood samples collected at 24 and 168h after AMPB treatment were used in this analysis. Kidney enzymes include: total bilirubin (TBIL), creatinine (CREA), urea nitrogen (BUN), and total protein (TP).
**Significantly different than control ($p < 0.05$)*

3.3. Identification of Gene Expression Changes

The gene expression profile of a biological system is highly dynamic in that it represents a snapshot of a system at a particular time point in response to external stimuli or insults. However, gene expression changes can occur as early or late events after chemical exposure. In this study, gene expression changes were investigated at 96 hr (HPA and D-serine) or 168 hr (PUR and AMPB) after nephrotoxin exposure.

3.3.1. HPA Treatment

Gene expression changes in the kidney isolated from rats 4 days after HPA exposure were identified using a t-test. Initially, gene expression changes at each dose compared to the control group were identified. To increase the stringency of the analysis, only the probe sets with $p<0.05$ over at least two consecutive doses were considered as significantly changed. As shown in Table 6, the number of probe sets meeting this criterion increases significantly when the dose of HPA reaches $\geq$750 mg/kg. The probe sets with significant expression changes across the entire dose range were then pooled to create a final list of a total of 212 probe sets. A search of the DAVID databases revealed that six genes were represented by two probe sets resulting in a total of 206 unique genes in the final gene list. The Affymetrix ID, the name/description of the genes with significant expression changes in the kidney after HPA treatment are presented in Supplemental Data Table S1.

Table 6: Renal Gene Expression Changes after HPA Treatment

Dose (mg/kg)	5	50	500	750	1000	1250
Number of Genes with Significant Changes in Expression Level	138	26	87	453	296	114
	22					
		1				
			5			
				179		
					83	
	212					

Gene expression changes in the kidneys of HPA-treated rats were identified using t-test ($p \leq 0.05$ over two consecutive doses).

To identify gene groups with similar dose response in terms of gene expression changes resulting from HPA treatment, the expression profiles of the final probe list were used as input data in a Self Organizing Map (SOM) clustering analysis. As shown in Figure 3, these genes can be grouped into two clusters of unique dose response patterns, although both clusters showed overall down-regulated gene expression.

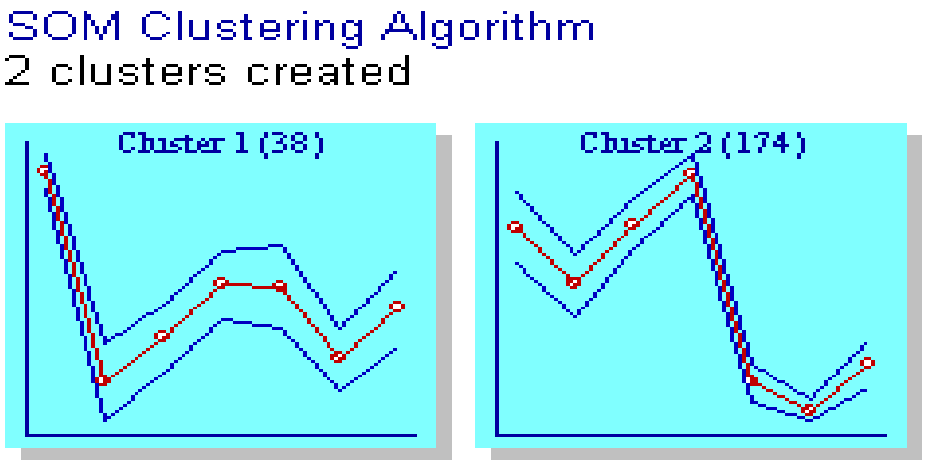

Figure 3: The 212 probe sets identified as differentially expressed after HPA treatment were subjected to Self Organizing Map (SOM) Clustering Analysis.
Dots represent HPA doses (i.e., 0, 5, 50, 500, 750, 1,000, and 1,250 mg/kg). Red line represents the average gene expression level across the dose range, while blue lines represent standard deviation of the relative gene expression levels.

To gain biological insights into the gene expression changes resulting from HPA exposure, the differentially expressed genes were used as input data to search the biological annotation databases of DAVID. This analysis revealed that a large number of biological processes and pathways were enriched (i.e. over-represented) in the final gene list. Among the enriched biological processes are cell cycle regulation, mitotic sister chromatid segregation, transcription regulation, and mRNA metabolism, processing, splicing and transport (Table 7). Although these biological processes are not unique to the functions of the kidney, perturbation of

essential cellular pathways, such as transcription regulation and mRNA processing/splicing/transport in the kidney, would likely have a significant impact on renal functions. In addition, down-regulation of genes involved in cell cycle progression and mitotic sister chromatid segregation might hinder compensatory cell proliferation during tissue repair. The entire list of gene ontology categories and KEGG pathways affected by HPA treatment and the statistical significance as determined by the DAVID analysis is shown in Supplemental Data Table S2.

Table 7: Enrichment of Biological Processes and Pathways Resulting from HPA-Induced Renal Differential Gene Expression

Category	Term	Count	P-Value
GOTERM_BP_ALL	biopolymer metabolism	28	4.20E-02
GOTERM_BP_ALL	cellular physiological process	89	1.50E-02
GOTERM_BP_ALL	chromosome segregation	4	3.80E-03
GOTERM_BP_ALL	mitotic sister chromatid segregation	3	1.40E-02
GOTERM_BP_ALL	mRNA metabolism	9	2.10E-04
GOTERM_BP_ALL	mRNA processing	7	2.60E-03
SP_PIR_KEYWORDS	mRNA transport	3	3.50E-03
GOTERM_BP_ALL	nucleobase, nucleoside, nucleotide and nucleic acid metabolism	36	6.10E-04
GOTERM_BP_ALL	regulation of cell cycle	9	4.90E-02
GOTERM_BP_ALL	regulation of cellular metabolism	22	2.70E-02
GOTERM_BP_ALL	regulation of cellular physiological process	35	1.30E-02
GOTERM_BP_ALL	regulation of cellular process	36	2.70E-02
GOTERM_BP_ALL	regulation of metabolism	24	1.70E-02
GOTERM_BP_ALL	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	22	6.20E-03
GOTERM_BP_ALL	regulation of physiological process	36	2.60E-02
GOTERM_BP_ALL	regulation of progression through cell cycle	9	4.80E-02
GOTERM_BP_ALL	regulation of RNA metabolism	3	1.80E-02
GOTERM_BP_ALL	regulation of transcription	20	2.00E-02
GOTERM_BP_ALL	regulation of transcription, DNA-dependent	20	7.40E-03
GOTERM_BP_ALL	RNA metabolism	11	2.70E-03
GOTERM_BP_ALL	RNA processing	9	4.70E-03
GOTERM_BP_ALL	RNA splicing	5	3.50E-02
GOTERM_BP_ALL	sister chromatid segregation	3	1.40E-02
GOTERM_BP_ALL	Transcription	21	2.50E-02
GOTERM_BP_ALL	transcription, DNA-dependent	20	1.60E-02

Biological processes/pathways, the number of genes involved in each of these processes and pathways. Statistical significance of enrichment shown in the table was based on the result of the search of the NIAID DAVID databases.

To visualize the effect of HPA treatment on gene expression in specific cellular pathways, GenMAPP analysis was performed using the expression profiles of the differentially expressed genes as input data. Representative pathways, as well as the number of genes involved in various cellular pathways and the direction of these gene expression changes are

shown in Table 8. Consistent with the results of the gene ontology analysis described above, pathways related to cell cycle regulation, gene transcription and mRNA processing/splicing were affected by HPA treatment (Table 8). Additionally, down-regulation of several ion transport pathways including anion transport, metal ion transport, etc. was observed in this analysis. The entire list of pathways and the direction of the gene expression changes involved in these pathways are provided in the Supplemental Data Table S3.

Table 8: Number of Up- and Down-regulated Genes Involved in Various Pathways after HPA Treatment

Category	Pathway	Down-regulated Genes	Up-regulated Genes
Molecular Function	ATPase activity	2	0
	Binding	2	0
	Carbohydrate Binding	2	0
	Cation channel activity	4	0
	Electrochemical potential-driven transport activity	3	0
	Magnesium ion binding	4	0
	phospheric ester hydrolase activity	2	0
	porter activity	2	0
	potassium channel activity	2	0
	Protein serine/ threonin kinase activity	4	0
	RNA binding	3	0
	signal trasducer activity	3	0
	Voltage-gated ion channel activity	2	0
cellular Component	GTPase regulator activity	2	0
Biological Process	Anion transport	3	0
	Deveopment	2	0
	Intracelllular protein transport	2	0
	intracellular signaling cascade	4	0
	Ion Transport	5	0
	Metal ion transport	6	0
	Morphogenesis	2	0
	nervous system development	2	0
	potassium ion transport	3	0
	regulation of progression thru cell cycle	4	0
	RNA processing	2	0
	system development	2	0
	transcription	5	0
	vesicle-mediated transport	2	0

The number of up- and down-regulated genes involved in the pathways under the three categories, i.e. molecular functions, cellular processes, and biological processes in the GenMAPP Pathway Database are shown.

The biological interaction of the differentially expressed genes and their potential partners was explored using PathwayArchitect. The network map of all molecular interactions is shown in Figure 4 and summarized in Table 9. This network map encompasses a variety of nodes such as cellular processes, small molecules and genes/proteins. There are three cellular process nodes: cell growth, apoptosis and homeostasis. Of these nodes, apoptosis is the most highly connected; it is associated with 12 genes/proteins that are all down-regulated. Interestingly, two genes, Sqstm1 (sequestosome 1 or oxidative stress induced) and Irf3 (interferon regulatory factor 3) form multiple connections with the apoptosis node. Cell growth is also highly connected with associations with eight down-regulated genes. Three genes, Igf1r (insulin-like growth factor 1 receptor), Col18a1 (collagen, type xviii, alpha 1) and Vegfa (vascular endothelial growth factor A), are connected to both apoptosis and cell growth nodes.

A small molecule node, Ca^{2+}, was also captured in this network. It forms a subnetwork with eight genes: Igfr1, Vegfa, Ak3 (adenylate kinase 3), Kcnt1 (potassium channel, subfamily T, member 1, or Slack), Scnn1a (sodium channel, nonvoltage-gated, type I, alpha), Dgka (diacylglycerol kinase, alpha), Sv2b (synaptic vesicle glycoprotein 2b), and Homer1 (homer homolog 1 (Drosophila)). It is noteworthy that Vegfa and Homer1 form multiple connections with Ca^{2+}.

Of the forty-four gene/protein nodes captured in this network map, 38 nodes showed expression changes after HPA treatment, while six showed no differential expression. Consistent with the result described above, 37 of the 38 differentially expressed genes were down-regulated. Scnn1a (sodium channel, nonvoltage-gated, type I, alpha) was the only up-regulated gene/protein node. Several highly connected gene/proteins nodes in this map function as the "central hubs" of this network. Quite unexpectedly, most of these "central hubs" showed no differential expression after HPA treatment. For instance, Hnf4 (hepatocyte nuclear factor 4, alpha) and Taf1 (TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor) are the most highly connected and are associated with 12 and 10 gene/protein nodes, respectively. Although both Hnf4 and Taf1 showed no differential expression, all the genes/proteins connected to them were down-regulated after HPA treatment. Of the differentially expressed genes, Hnrnpa1 (also known as Hnrpa1, heterogeneous nuclear ribonucleoprotein A1) and Sfrs2 (splicing factor, arginine/serine-rich 2) are relatively highly connected. Besides being connected to apoptosis, all the genes/proteins connected to these nodes showed no differential expression after HPA treatment.

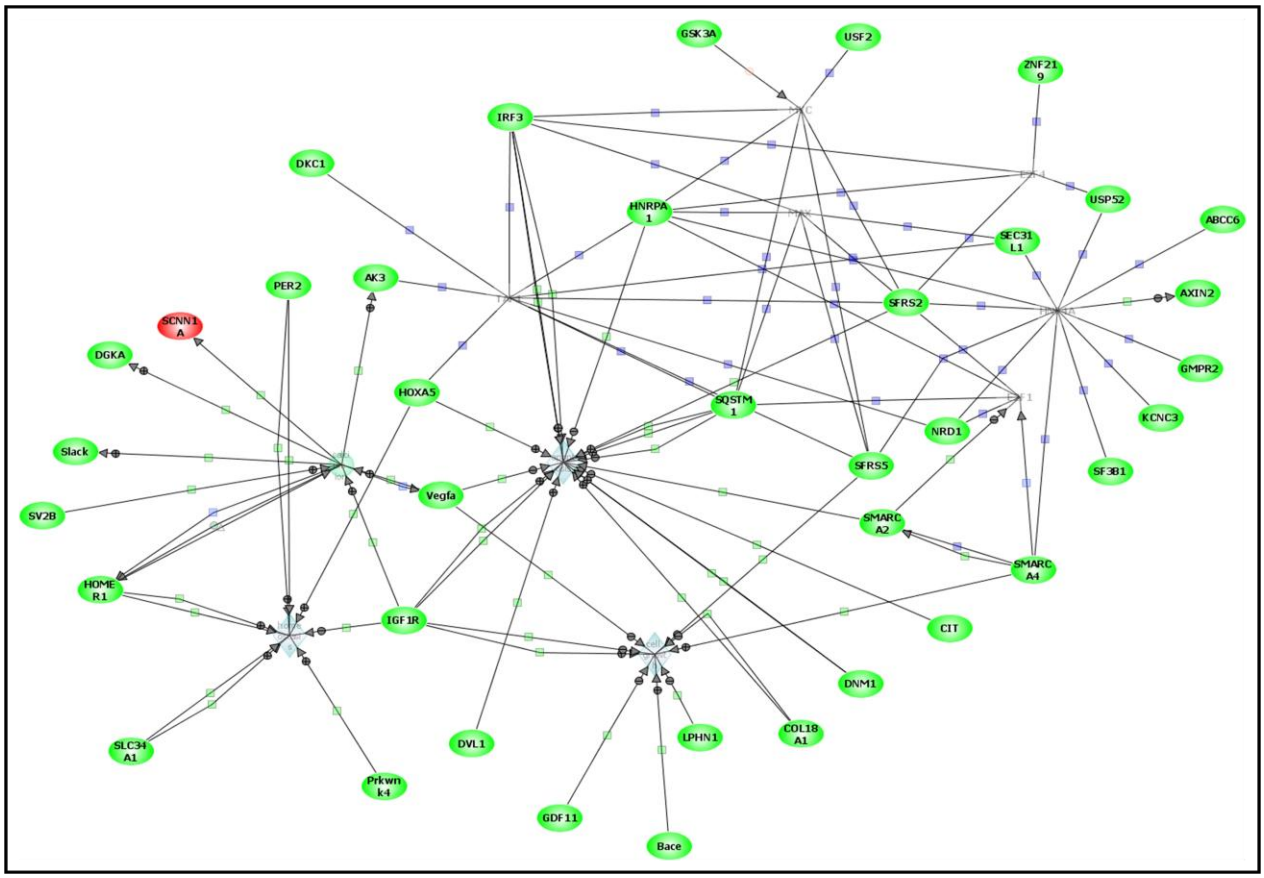

Figure 4: HPA-Induced Renal Differential Gene Expression Involved in the Biological Association Network of all Molecular Interactions.

Table 9: Direction of Expression Changes Involved in the Biological Association Network of all molecular interactions after HPA Treatment

Gene	Gene Description	Direction
SCNN1A	sodium channel, nonvoltage-gated 1 alpha	up
ABCC6	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	down
AK3	adenylate kinase 3	down
AXIN2	axin 2 (conductin, axil)	down
Bace	beta-site APP cleaving enzyme	down
CIT	citron (rho-interacting, serine/threonine kinase 21)	down
COL18A1	collagen, type XVIII, alpha 1	down
DGKA	diacylglycerol kinase, alpha 80kDa	down
DKC1	dyskeratosis congenita 1, dyskerin	down
DNM1	dynamin 1	down
DVL1	dishevelled, dsh homolog 1 (Drosophila)	down
E2F1	E2F transcription factor 1	down
E2F4	E2F transcription factor 4, p107/p130-binding	down

GDF11	growth differentiation factor 11	down
GMPR2	guanosine monophosphate reductase 2	down
GSK3A	glycogen synthase kinase 3 alpha	down
HNF4A	hepatocyte nuclear factor 4, alpha	down
HNRPA1	heterogeneous nuclear ribonucleoprotein A1	down
HOMER1	homer homolog 1 (Drosophila)	down
HOXA5	homeo box A5	down
IGF1R	insulin-like growth factor 1 receptor	down
IRF3	interferon regulatory factor 3	down
KCNC3	potassium voltage-gated channel, Shaw-related subfamily, member 3	down
LPHN1	latrophilin 1	down
MAX	MYC associated factor X	down
MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	down
NRD1	nardilysin (N-arginine dibasic convertase)	down
PER2	period homolog 2 (Drosophila)	down
Prkwnk4	protein kinase, lysine deficient 4	down
SEC31L1	SEC31-like 1 (S. cerevisiae)	down
SF3B1	splicing factor 3b, subunit 1, 155kDa	down
SFRS2	splicing factor, arginine/serine-rich 2	down
SFRS5	splicing factor, arginine/serine-rich 5	down
Slack	potassium channel subunit (Slack)	down
SLC34A1	solute carrier family 34 (sodium phosphate), member 1	down
SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	down
SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	down
SQSTM1	sequestosome 1	down
SV2B	synaptic vesicle glycoprotein 2B	down
TAF1	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 250kDa	down
USF2	upstream transcription factor 2, c-fos interacting	down
USP52	ubiquitin specific peptidase 52	down
Vegfa	vascular endothelial growth factor A	down
ZNF219	zinc finger protein 219	down

The genes involved in the biological association network of all molecular interactions determined using PathwayArchitect are shown.

The directions of the expression changes of the gene/protein nodes in this network map are also shown.

3.3.2. D-Serine Treatment

Gene expression changes were identified using two different statistical methods, namely t-test and ANOVA. Initially, gene expression changes at each dose compared to control were identified by t-test. To account for the multiple testing nature of DNA microarrays, only gene expression changes with $p<0.01$ over two consecutive doses were considered as differentially expressed. Table 10 shows the result of the t-test, in which 1946 and 1520 genes were found to be up-regulated and down-regulated, respectively. The dataset was also analyzed using ANOVA with Bonferroni correction for multiple testing ($p<0.01$), which identified 2172 genes as differentially expressed. To increase the stringency of the statistical analysis (and thus the quality of the result), only the genes that were commonly identified in both t-test and ANOVA were included in the final gene list. This resulted in the identification of 1158 up-regulated and 749 down-regulated genes. The Affymetrix ID and the gene name/description of the entire list of the differentially expressed genes (i.e. 1907 genes) are presented in Supplemental Data Table S4.

Table 10: Renal Gene Expression Changes after DSER Treatment

Dose of D-serine	**5 mg/kg**	**20 mg/kg**	**50 mg/kg**	**200 mg/kg**	**500 mg/kg**
# of up-regulated genes (p < 0.01)	365	222	100	2131	2615
# of common up-regulated genes (p < 0.01) over two dose levels	115				
		27			
			63		
				1741	
Total (common up-regulated genes)	**1946**				
# of down-regulated genes (p < 0.01)	11	206	181	1446	1538
# of common down-regulated genes (p < 0.01) over two dose levels	0				
		82			
			130		
				1308	
Total (common down-regulated genes)	**1520**				

Gene expression changes were identified using t-test (p<0.01 over two consecutive doses).

To identify gene groups with similar dose-response in term of expression changes to D-serine treatment, the expression profiles of the entire list of the 1907 differentially expressed genes were used an input data in a SOM clustering analysis. Similar to the result of HPA treatment, only two tight clusters, one with all 1158 up-regulated genes and the other with all 749 down-regulated genes, were obtained, indicating that all the up-regulated genes, as well as all the down-regulated genes, have a unified dose-response profile. Changing the parameters used in the analysis did not change the number of gene clusters. For instance, setting the parameter to generate 4 clusters resulted in 2 empty clusters (Cluster 2 and 3 in Figure 5). This result indicates that this homogenous dose-response pattern is independent of the parameters used in the SOM analysis.

Based on the expression profiles of these genes clusters, there appears to be minimal changes in the gene expression levels at lower doses (5, 20 and 50 mg/kg), while the most

significant changes in the expression levels were observed at 200 and 500 mg/kg in both the up- (Cluster 1) and the down-regulated directions (Cluster 4). However, it should be noted that the up- and down-regulation of 52 and 101 genes, respectively, in the dose range of 5-50 mg/kg did reach the statistical significance threshold.

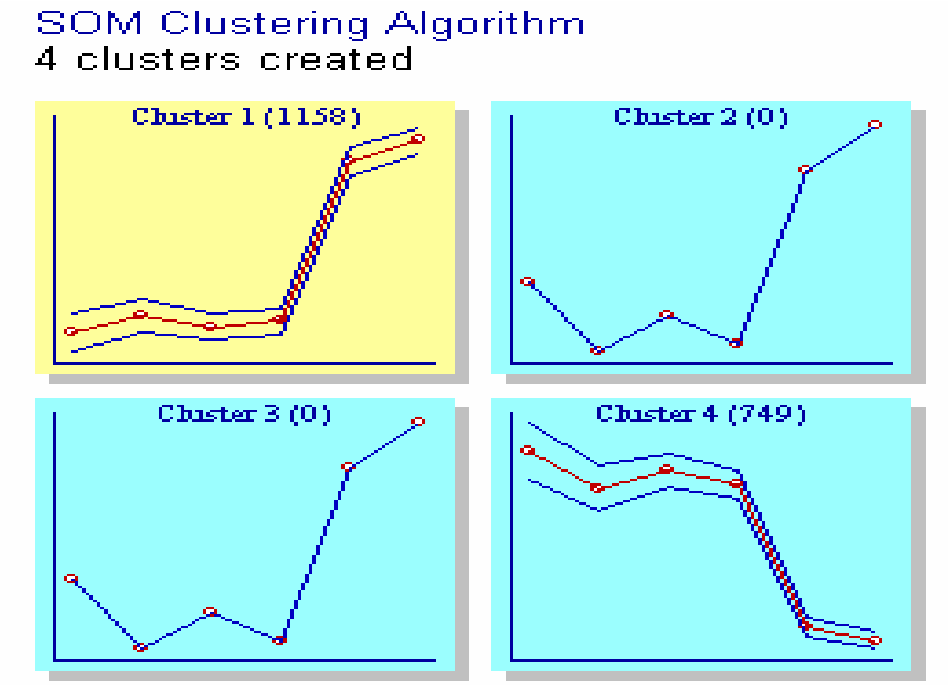

Figure 5: Self Organizing Map Clustering Analysis of the Differentially Expressed Genes Resulting from D-Serine Exposure.

The result of self organizing map clustering analysis of the entire list of 1907 differentially expressed genes is presented. Each cluster displays the cluster number and the number of cluster members (# in parenthesis). Cluster 1 and 4 represent 1158 and 749 up- and down-regulated genes, respectively. Note that Clusters 2 and 3 are empty clusters with zero genes. The x-axis and y-axis represent the doses of D-serine (the dots on the middle line: 0, 5, 20, 50, 200 and 500 mg/kg) and the normalized expression level (zero means and unit variance), respectively. The middle red line represents the average gene expression pattern for the cluster. The two outer blue lines represent the standard deviation of the expression level.

To gain biological insights into the gene expression changes resulting from D-serine exposure, the 1158 up-regulated and 749 down-regulated genes were used separately to search the biological annotation database under the National Institute of Allergy and Infectious Diseases (NIAID) Database for Annotation, Visualization, and Integrated Discovery (DAVID) web site. This analysis identified a large number of biological processes that were enriched (i.e. genes involved in these pathways were over-represented) in these gene lists, indicating that these pathways were specifically affected by D-serine exposure. Detailed examination of the result revealed that actin cytoskeleton biogenesis and organization, apoptosis, cell adhesion, cell cycle regulation, chromatin assembly, excision repair of damaged DNA, DNA replication and packaging, protein metabolism and transport, inflammatory response, proteasome-mediated

degradation of oxidatively damaged cytosolic proteins, Ras protein signal transduction, TGF-beta signaling pathway, translation initiation/elongation and mRNA transcription, processing, splicing and transport were up-regulated. On the other hand, major cellular metabolic pathways including carbohydrate metabolism, TCA cycle, oxidative phosphorylation, ATP synthesis coupled electron transport, amino acid metabolism and transport, lipid metabolism, nucleotide metabolism, and vitamin metabolism were down-regulated. In addition, compensatory oxidative stress response (induction of antioxidant genes and glutathione metabolism) and angiotensin I converting enzyme (ACE) pathways were also down-regulated. The result of this analysis is summarized in Table 11.

To investigate the biological processes and pathways selectively affected by low-dose D-serine treatment, the 52 up-regulated and 101 down-regulated genes identified in the dose range of 5 – 50 mg/kg were used in a similar analysis. Interestingly, genes involved in amino acid metabolism/transport, glutathione metabolism, lipid metabolism, nucleotide metabolism, oxidative phosphorylation, and vitamin metabolism were over-represented among the down-regulated genes, while those involved in actin cytoskeleton biogenesis/organization and intracellular protein transport were over-represented among the up-regulated genes (i.e. the biological processes/pathways marked with an asterisk in Table 11). This result thus suggests that down-regulation of major cellular metabolic pathways (especially those related to energy metabolism) and glutathione metabolism already occurs when there is no detectable abnormality using traditional techniques like clinical chemistry and histopathological analysis. The entire list of biological processes and pathways affected by D-serine treatment is shown in the Supplemental Data Table S5.

Table 11: Consolidated list of Enriched Biological Processes/Pathways Resulting from D-Serine Treatment

Biological Process/Pathway	Change Direction
actin cytoskeleton organization and biogenesis*	Up
annexin (exocytosis and endocytosis)	Up
cell communication	Up
cell organization and biogenesis*	Up
cellular protein metabolism	Up
chromatin assembly	Up
DNA damage and excision repair	Up
DNA replication and packaging	Up
focal adhesion	Up
Inflammatory Response	Up
intracellular protein transport*	Up
microtubule cytoskeleton organization and biogenesis	Up
mRNA transcription, processing, splicing and transport	Up
nucleobase, nucleoside, nucleotide and nucleic acid metabolism	Up
nucleosome assembly	Up

proteasome Pathway (degradation of oxidatively damaged cytosolic proteins)	Up
protein complex assembly	Up
ras protein signal transduction	Up
regulation of apoptosis	Up
regulation of progression through cell cycle	Up
TGF-beta Signaling Pathway	Up
tight junction	Up
translational initiation	Up
amino acid transport and metabolism*	Down
angiotensin 1 converting enzyme (ACE) Pathway	Down
ATP synthesis coupled electron transport	Down
carbohydrate metabolism	Down
carboxylic acid metabolism and transport*	Down
coenzyme metabolism*	Down
glutathione metabolism*	Down
glycolysis / gluconeogenesis	Down
lipid metabolism*	Down
nucleotide metabolism*	Down
oxidative phosphorylation*	Down
oxidative stress (induction of antioxidant genes)	Down
tricarboxylic acid cycle	Down
vitamin metabolism*	Down

The 1158 up-regulated and 749 down-regulated genes were used to search the NIAID DAVID biological annotation database separately.
A consolidated list of the biological processes/pathways over-represented in these gene lists and their change directions are shown.
**Biological processes/pathways significantly affected by low dose D-serine treatment (5 – 50 mg/kg).*

To visualize the effect of D-serine treatment on gene expression concerning specific cellular pathways, GenMAPP analysis was performed using the expression profiles of the 1907 differentially expressed genes as input data. Representative pathways, as well as the number of genes involved in these pathways and the direction of their expression changes are shown in Table 12. Consistent with the result of gene ontology analysis shown above, a large number of genes involved in apoptosis, cell cycle regulation, MAP Kinase signaling cascade, transcription initiation, mRNA processing, protein translation, integrin-mediated cell adhesion, actin cytoskeleton, TGF-β signaling, inflammatory response and ubiquitin proteasome pathway were up-regulated after D-serine treatment. In contrast, cholesterol biosynthesis, electron transport chain, glucocorticoid metabolism, steroid biosynthesis, fatty acid metabolism, TCA cycle,

glycolysis/gluconeogenesis, and oxidative stress response were down-regulated. Two representative pathways, cell cycle control and electron transport chain are shown in Figure 6 and Figure 7, respectively. In the cell cycle regulation pathway, 15 genes were up-regulated, while only one gene was down-regulated (Figure 6). In contrast, eleven genes were down-regulated in the electron transport chain pathway, whereas only one gene was up-regulated (Figure 7). The entire lists of pathways and the change direction of the genes involved in these pathways are provided in the Supplemental Data Table S6.

Table 12: Pathway Analysis of Differential Gene Expression Induced by D-Serine Treatment

Category	Pathway	Up-Regulated Genes	Down-Regulated Genes
Cellular Processes	Apoptosis	8	1
	Cell cycle control	15	1
	MAPK Cascade	2	1
	Eukaryotic Transcription Initiation	4	0
	Translations Factors	6	0
	G13 Signaling Pathway	6	0
	Apoptosis Modulation by HSP70	6	1
	mRNA processing	10	0
	Signal Transduction of S1 Receptor	2	0
	Wnt Signaling Pathway	2	1
	DNA Replication	2	0
	G Protein Signaling Pathways	9	1
	Integrin-mediated cell adhesion	6	2
	Regulation of actin cytoskeleton	18	3
	TGF-beta signaling pathway	6	1
Metabolic Processes	Cholesterol Biosynthesis	0	1
	Electron Transport Chain	1	11
	Pentose Phosphate Pathway	2	0
	Fatty Acid Degradation	1	3
	Glycogen Metabolism	2	2
	TCA Cycle	0	8
	Prostaglandin Synthesis and Regulation	5	1
	Fatty Acids Synthesis	2	4
	Glycolysis and Gluconeogenesis	4	6
	Mitochondrial LC-Fatty Acid Beta-Oxidation	1	3
Molecular Function	Nuclear Receptors	0	3
	Matrix Metalloproteinases	4	1
	Cytoplasmic Ribosomal Proteins	45	0
Physiological Processes	Calcium Regulation in the Cardiac Cell	17	2
	Inflammatory Response Pathway	7	1
	Myometrial Relaxation and Contraction Pathways	19	2

	ACE Inhibitor Pathway	0	2
	Oxidative Stress	2	4
	Striated Muscle Contraction	4	0
	Complement Activation, Classical Pathway	5	4
	Proteasome Degradation	14	0

Number of differentially expressed genes involved in representative pathways was determined using GenMAPP (version 2.0).

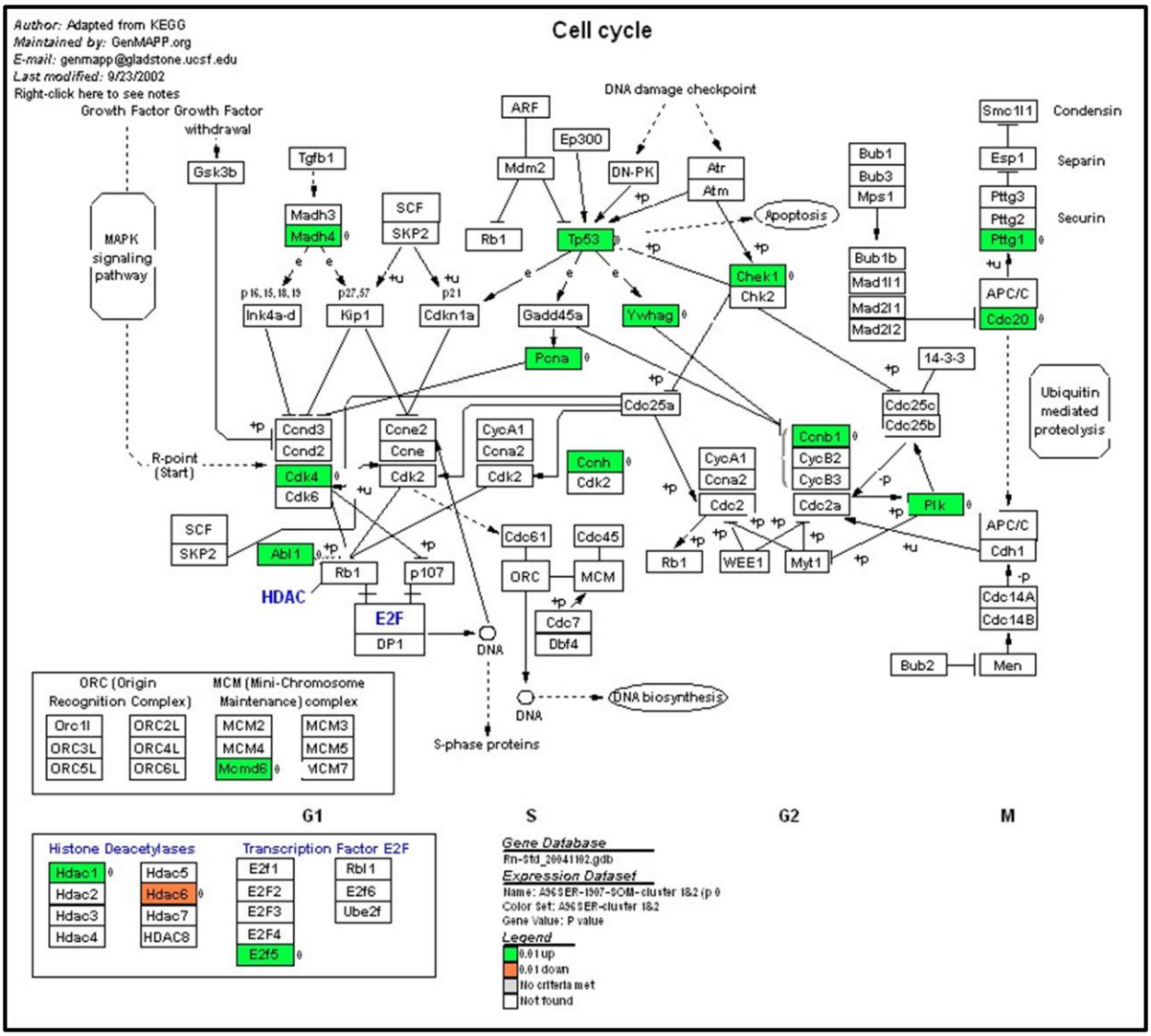

Figure 6: Gene expression changes involved in the cell cycle regulation.
The expression profiles of the entire list of 1907 differentially expressed genes were used as input data in GenMAPP analysis. There were 15 genes up-regulated (green), while only one gene was down-regulated (orange) in this pathway.

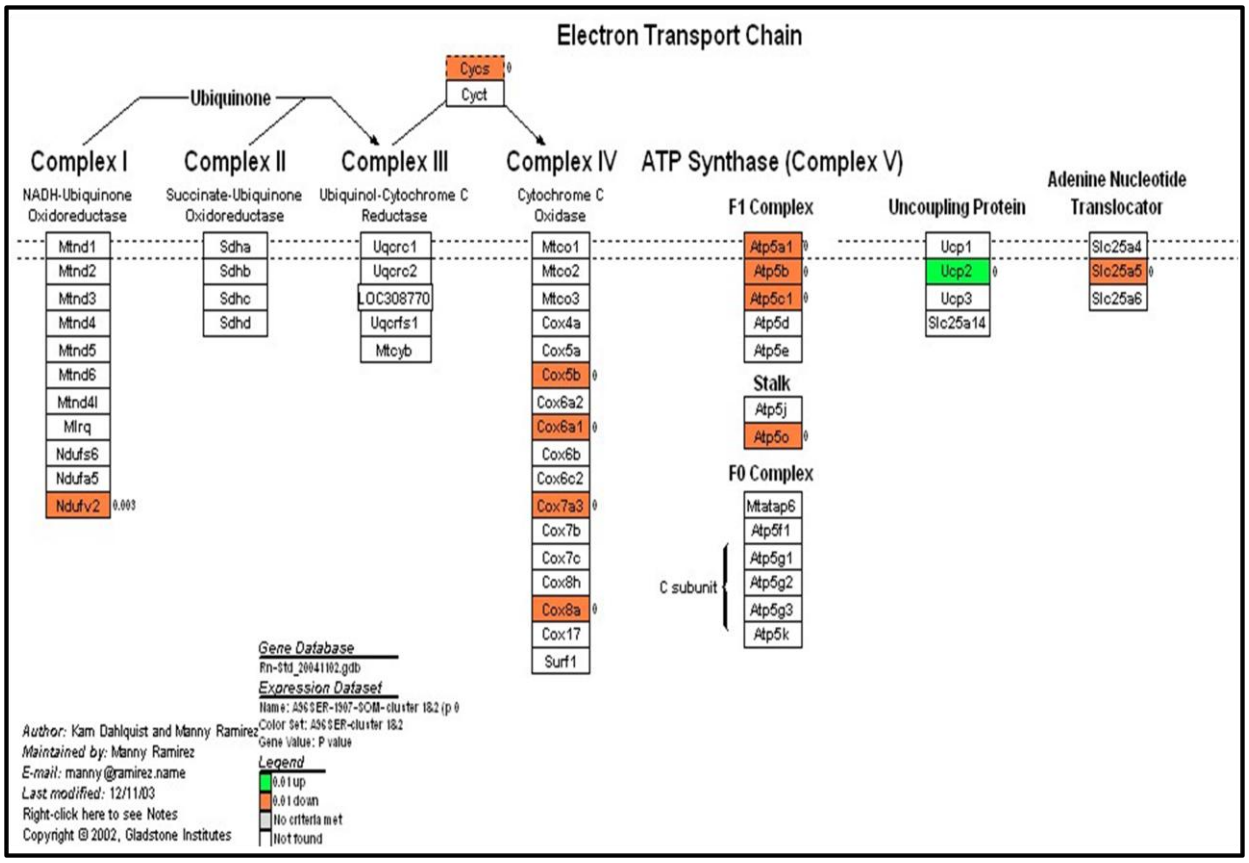

Figure 7: Gene expression changes involved in the electron transport chain.
The expression profiles of the entire list of 1907 differentially expressed genes were used as input data in GenMAPP analysis. There were 11 genes down-regulated (orange), while only one gene was up-regulated (green) in this pathway.

Biological association networks of the differentially expressed genes were generated using the software tool PathwayArchitect, which contains a database of biological association of physical and functional interactions involving proteins, small molecules, enzymes, protein families, etc. based on the mining of the literature. The wide coverage of this database can potentially provide novel insights into functional interactions between the differentially expressed genes (as well as their interaction with the genes that shows no differential expression), which may not be easily identified using other traditional methods. Using this software tool on the entire list of 1907 differentially expressed genes, we were able to identify functional interactions between various genes in response to D-serine exposure regarding promoter binding, regulation, transport, expression, post-translational modifications, and binding complex formation. For instance, connections between transcription factors (such as MYC, NFκB and EGR1) and ECM components including (type I collagen, alpha 1 and 2, fibronectin 1 and fibrillin 1) are observed in the promoter binding network. Besides the regulation of the ECM components by these transcription factors, the regulation of these ECM components by matrix metalloproteases (MMPs) and tissue inhibitor of metalloproteinases (TIMPs) are also

captured in the regulation network. Additionally, the connections between IER3 (immediate early response 3), MCL1 (myeloid cell leukemia sequence 1, a member of the BCL2 family), TNFRSF1A (tumor necrosis factor receptor superfamily, member 1A), caspase 3 and P53, which are related to the apoptotic pathway, are also observed in this network. As shown in Table 13, there are a large number of differentially expressed genes (31-118 genes) involved in these biological association networks. The entire list of the genes involved in these networks and the direction of their expression changes are provided in the Supplemental Data Table S7.

Table 13: Biological Association of Networks of Differentially Expressed Genes Resulting from D-Serine Treatment

Biological Association Network	Up-Regulated Genes	Down-Regulated Genes
Promoter Binding	29	12
Regulation	78	40
Transport	59	39
Protein Modification	53	14
Expression	31	8
Complex Binding	25	6

The entire list of 1907 differentially expressed genes was used as input data in PathwayArchitect (version 2.0.1) analysis.

A list of biological association networks, as well as the number of up- and down-regulated genes involved in each of these networks constructed using PathwayArchitect are shown.

3.3.3. PUR treatment

Gene expression changes in the kidneys isolated from rats 7 days after PUR exposure were identified using two statistical methods. Initially, ANOVA with adjusted Bonferroni correction for multiple testing was performed. The result of this analysis revealed that the expression of 1569 genes (represented by 1635 probe sets) was significantly altered by the PUR treatment. Data analysis using the significance analysis of microarrays method (SAM, Tusher et al., 2001) module of the TIGR Multi-experiment Viewer software (version 4.0) revealed differential expression of 1219 genes (represented by 1278 probe sets) after PUR treatment. To further increase the stringency of the analysis, the results of ANOVA and SAM were compared, and only the genes that were commonly identified in both analyses were considered as differentially expressed. This resulted in a final list of 1127 genes (1177 probe sets) that showed gene expression changes resulting from PUR treatment.

To identify gene groups with similar dose response to PUR treatment in terms of gene expression changes, the expression profiles of the final gene list was used as input data in SOM clustering analysis. As shown in Figure 8, two tight clusters of unique dose response patterns were obtained. Cluster 1 consists of 380 down-regulated genes (represented by 388 probe sets), while Cluster 2 contains 747 up-regulated genes (represented by 789 probe sets). In both clusters, the dose of 25 mg/kg appears to be a transition point. While the degree of gene expression changes was relatively small at doses <25 mg/kg, a much larger magnitude of gene

expression changes can be observed beyond this dose. The Affymetrix ID, the name/description of the genes, and the change direction of the genes in each cluster are presented in Supplemental Data Table S8.

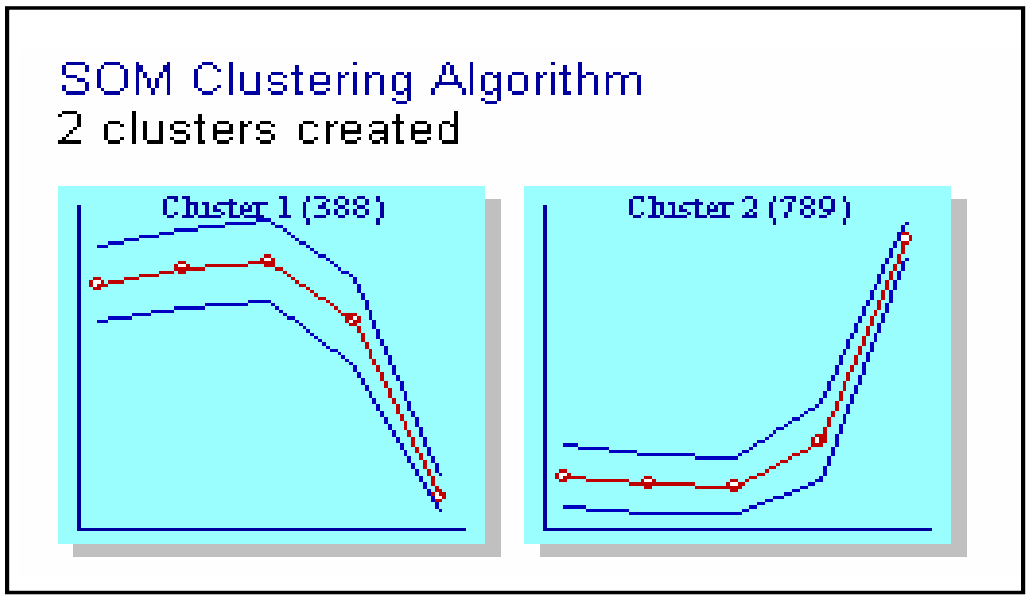

Figure 8: Self-Organizing Map (SOM) Clustering.
The expression profiles of 1177 differentially expressed probe sets (encoding 1125 genes) were used as input data in SOM clustering analysis. The results of this analysis revealed that these genes could be grouped into two clusters. Note that the differentially expressed genes were clustered as up- or down-regulated in response to PUR treatment. The number of probe sets in each cluster is shown (# in parenthesis). The x-axis and y-axis represent the doses of PUR and the normalized expression level (zero means and unit variance), respectively. The middle red line represents the average expression level for the cluster. The dots on the middle red line correspond to the doses of PUR (0, 5, 25, 75, and 150 mg/kg). The two outer lines represent the standard deviation of the expression levels.

To gain biological insights into the gene expression changes resulting from PUR exposure, the lists of up and down-regulated genes were used to search the biological annotation databases of the NIAID DAVID website (http://david.abcc.ncifcrf.gov). This analysis revealed genes involved in a large number of biological processes and pathways were overpresentated among the differentially expressed genes (Table 14). Biological processes and pathways in which the genes were down-regulated are related to cellular metabolisms (including amino acid metabolism, lipid metabolism, carbohydrate metabolism, nucleotide metabolism, coenzyme metabolism, cofactor metabolism, hormone metabolism, and energy production), response to steroid hormone and insulin stimuli, response to xenobiotic stimulus (including xenobiotic metabolism and sulfur compound metabolism), and ion transport. On the other hand, biological processes and pathways in which the genes were up-regulated are related to cellular morphogenesis, actin cytoskeleton organization and biogenesis, acute inflammatory/immune response, wound healing and tissue remodeling, angiogenesis, regulation of cell death and

growth, chromosome biogenesis and organization (including DNA replication and packaging and establishment of chromatin architecture), protein synthesis, degradation (ubiquitin proteasome pathway) and transport, RNA transcript, processing, splicing and transport, and response to xenobiotic stimulus. The entire list of biological processes (and KEGG pathways) impacted by PUR treatment and the statistical significance as determined by DAVID analysis are shown in Supplemental Data Table S9.

Table 14: Consolidated list of Enriched Biological Processes/Pathways Resulting from Puromycin Treatment

Category	Term	Count	P-Value	Direction
GOTERM_BP_ALL	acetyl-CoA metabolic process	8	3.80E-04	Down
GOTERM_BP_ALL	amine metabolic process	37	6.20E-09	Down
GOTERM_BP_ALL	amino acid and derivative metabolic process	37	1.30E-09	Down
GOTERM_BP_ALL	aromatic compound metabolic process	17	6.30E-06	Down
GOTERM_BP_ALL	branched chain family amino acid catabolic process	3	2.50E-02	Down
GOTERM_BP_ALL	carboxylic acid metabolic process	59	2.20E-17	Down
GOTERM_BP_ALL	cellular lipid metabolic process	32	3.80E-04	Down
GOTERM_BP_ALL	cellular response to insulin stimulus	3	4.00E-02	Down
GOTERM_BP_ALL	coenzyme metabolic process	19	1.00E-05	Down
GOTERM_BP_ALL	cofactor metabolic process	22	3.90E-06	Down
GOTERM_BP_ALL	cysteine metabolic process	4	1.50E-03	Down
GOTERM_BP_ALL	dicarboxylic acid metabolic process	5	1.30E-03	Down
GOTERM_BP_ALL	electron transport	31	1.70E-07	Down
GOTERM_BP_ALL	fatty acid beta-oxidation	5	8.80E-03	Down
GOTERM_BP_ALL	fatty acid metabolic process	17	3.00E-04	Down
GOTERM_BP_ALL	flagellum biogenesis	3	1.20E-02	Down
SP_PIR_KEYWORDS	gluconeogenesis	6	8.30E-05	Down
GOTERM_BP_ALL	glycerol metabolic process	3	4.00E-02	Down
KEGG_PATHWAY	Glycine, serine and threonine metabolism	7	2.70E-03	Down
KEGG_PATHWAY	Glyoxylate and dicarboxylate metabolism	4	4.80E-03	Down
GOTERM_BP_ALL	hexose biosynthetic process	6	4.20E-03	Down
KEGG_PATHWAY	Histidine metabolism	4	3.70E-02	Down
GOTERM_BP_ALL	lipid metabolic process	35	6.80E-04	Down
GOTERM_BP_ALL	L-serine metabolic process	3	4.00E-02	Down
GOTERM_BP_ALL	male gamete generation	10	3.50E-02	Down
KEGG_PATHWAY	Metabolism of xenobiotics by cytochrome P450	14	2.60E-07	Down
GOTERM_BP_ALL	monocarboxylic acid metabolic process	30	7.20E-09	Down
GOTERM_BP_ALL	monosaccharide biosynthetic process	6	4.80E-03	Down
GOTERM_BP_ALL	nitrogen compound metabolic process	41	3.30E-10	Down
GOTERM_BP_ALL	nonprotein amino acid metabolic process	3	2.50E-02	Down
GOTERM_BP_ALL	nucleobase, nucleoside and nucleotide metabolic process	17	1.80E-03	Down
GOTERM_BP_ALL	nucleotide metabolic process	16	2.10E-03	Down

GOTERM_BP_ALL	organic anion transport	4	1.90E-02	Down
GOTERM_BP_ALL	oxaloacetate metabolic process	3	3.90E-03	Down
KEGG_PATHWAY	Pentose and glucuronate interconversions	9	5.90E-07	Down
KEGG_PATHWAY	Porphyrin and chlorophyll metabolism	10	2.00E-06	Down
KEGG_PATHWAY	PPAR signaling pathway	8	4.50E-02	Down
KEGG_PATHWAY	Propanoate metabolism	6	3.70E-03	Down
KEGG_PATHWAY	Pyruvate metabolism	9	3.70E-05	Down
GOTERM_BP_ALL	response to chemical stimulus	38	5.10E-03	Down
GOTERM_BP_ALL	response to hormone stimulus	14	5.80E-03	Down
GOTERM_BP_ALL	response to steroid hormone stimulus	9	3.50E-02	Down
GOTERM_BP_ALL	response to xenobiotic stimulus	5	2.00E-02	Down
GOTERM_BP_ALL	ribonucleotide biosynthetic process	7	1.60E-02	Down
GOTERM_BP_ALL	S-adenosylhomocysteine metabolic process	4	2.20E-02	Down
GOTERM_BP_ALL	serine family amino acid metabolic process	9	2.50E-06	Down
GOTERM_BP_ALL	sodium ion transport	8	5.00E-02	Down
KEGG_PATHWAY	Starch and sucrose metabolism	11	2.60E-06	Down
GOTERM_BP_ALL	sulfur amino acid metabolic process	7	1.00E-04	Down
GOTERM_BP_ALL	sulfur metabolic process	14	2.10E-06	Down
SP_PIR_KEYWORDS	Symport	9	2.00E-03	Down
GOTERM_BP_ALL	tricarboxylic acid cycle intermediate metabolic process	5	4.30E-03	Down
KEGG_PATHWAY	Tryptophan metabolism	9	2.90E-04	Down
KEGG_PATHWAY	Valine, leucine and isoleucine degradation	9	1.60E-04	Down
GOTERM_BP_ALL	vitamin metabolic process	11	2.00E-04	Down
GOTERM_BP_ALL	xenobiotic metabolic process	5	1.80E-02	Down
GOTERM_BP_ALL	actin polymerization and/or depolymerization	14	2.30E-06	Up
GOTERM_BP_ALL	anatomical structure development	148	2.00E-03	Up
GOTERM_BP_ALL	antigen processing and presentation	10	1.80E-02	Up
GOTERM_BP_ALL	blood vessel morphogenesis	18	3.20E-02	Up
KEGG_PATHWAY	Cell cycle	18	8.60E-04	Up
GOTERM_BP_ALL	cell death	60	1.90E-02	Up
GOTERM_BP_ALL	cell differentiation	115	1.80E-02	Up
GOTERM_BP_ALL	cell division	19	4.20E-04	Up
GOTERM_BP_ALL	cell migration	29	9.70E-03	Up
GOTERM_BP_ALL	cellular protein metabolic process	209	9.30E-09	Up
KEGG_PATHWAY	Complement and coagulation cascades	10	2.10E-02	Up
GOTERM_BP_ALL	cytoskeleton organization and biogenesis	43	1.70E-03	Up
GOTERM_BP_ALL	death	60	1.90E-02	Up
GOTERM_BP_ALL	DNA packaging	18	1.80E-02	Up
SP_PIR_KEYWORDS	DNA recombination	4	2.00E-02	Up
GOTERM_BP_ALL	DNA replication	21	4.50E-04	Up
KEGG_PATHWAY	ECM-receptor interaction	15	2.00E-04	Up

GOTERM_BP_ALL	establishment and/or maintenance of chromatin architecture	18	1.50E-02	Up
GOTERM_BP_ALL	establishment of cell polarity	4	2.40E-02	Up
GOTERM_BP_ALL	establishment of RNA localization	6	3.30E-02	Up
KEGG_PATHWAY	Focal adhesion	27	6.40E-04	Up
GOTERM_BP_ALL	gene expression	156	6.30E-05	Up
GOTERM_BP_ALL	hemopoietic or lymphoid organ development	19	4.50E-02	Up
GOTERM_BP_ALL	I-kappaB kinase/NF-kappaB cascade	13	4.00E-02	Up
GOTERM_BP_ALL	immune response	38	1.10E-02	Up
GOTERM_BP_ALL	intracellular protein transport	35	4.00E-02	Up
KEGG_PATHWAY	Leukocyte transendothelial migration	16	5.50E-03	Up
GOTERM_BP_ALL	modification-dependent protein catabolic process	16	8.30E-03	Up
SP_PIR_KEYWORDS	mRNA processing	14	3.20E-03	Up
SP_PIR_KEYWORDS	mRNA splicing	13	1.30E-03	Up
GOTERM_BP_ALL	mRNA transport	6	1.30E-02	Up
GOTERM_BP_ALL	muscle cell differentiation	9	2.60E-02	Up
GOTERM_BP_ALL	negative regulation of programmed cell death	27	7.00E-03	Up
GOTERM_BP_ALL	nuclear transport	18	1.80E-03	Up
GOTERM_BP_ALL	nucleic acid transport	6	3.30E-02	Up
GOTERM_BP_ALL	nucleocytoplasmic transport	17	3.40E-03	Up
GOTERM_BP_ALL	phosphate transport	9	2.60E-02	Up
GOTERM_BP_ALL	positive regulation of actin filament polymerization	4	6.80E-03	Up
GOTERM_BP_ALL	positive regulation of angiogenesis	6	1.10E-03	Up
SP_PIR_KEYWORDS	protein biosynthesis	45	4.80E-16	Up
SP_PIR_KEYWORDS	protein degradation	4	8.10E-03	Up
GOTERM_BP_ALL	protein import into nucleus	12	8.40E-03	Up
GOTERM_BP_ALL	protein polymerization	21	1.50E-11	Up
GOTERM_BP_ALL	protein-RNA complex assembly	15	4.20E-04	Up
GOTERM_BP_ALL	proteolysis	50	6.40E-03	Up
GOTERM_BP_ALL	regulation of actin filament polymerization	10	8.80E-08	Up
GOTERM_BP_ALL	regulation of cytoskeleton organization and biogenesis	13	5.70E-06	Up
GOTERM_BP_ALL	regulation of protein metabolic process	32	2.10E-04	Up
GOTERM_BP_ALL	response to stress	86	7.80E-03	Up
GOTERM_BP_ALL	response to wounding	42	2.60E-02	Up
GOTERM_BP_ALL	ribonucleoprotein complex biogenesis and assembly	19	4.20E-04	Up
KEGG_PATHWAY	Ribosome	28	4.10E-11	Up
GOTERM_BP_ALL	RNA processing	27	1.20E-02	Up
GOTERM_BP_ALL	RNA splicing	18	4.00E-03	Up
GOTERM_BP_ALL	RNA transport	6	3.30E-02	Up
GOTERM_BP_ALL	tissue remodeling	18	3.20E-02	Up
KEGG_PATHWAY	Toll-like receptor signaling pathway	14	3.90E-03	Up
GOTERM_BP_ALL	transcription from RNA polymerase I promoter	4	2.40E-02	Up

GOTERM_BP_ALL	translation	68	7.30E-13	Up
GOTERM_BP_ALL	ubiquitin-dependent protein catabolic process	16	7.60E-03	Up
SP_PIR_KEYWORDS	ubl conjugation	21	3.40E-02	Up
GOTERM_BP_ALL	wound healing	19	2.10E-02	Up

The 747 up-regulated and 380 down-regulated genes were used to search the NIAID DAVID biological annotation database separately.
A consolidated list of the biological processes/pathways over-represented in these gene lists and their change directions are shown.

Consistent with the gene ontology analysis results, pathway analysis (using GenMAPP) confirmed that eleven genes directly involved in mRNA processing and six accessory proteins were up-regulated after PUR treatment (Figure 9). Of these genes, five genes belong to the heterogeneous nuclear ribonucleoprotein family, which functions as RNA binding proteins.

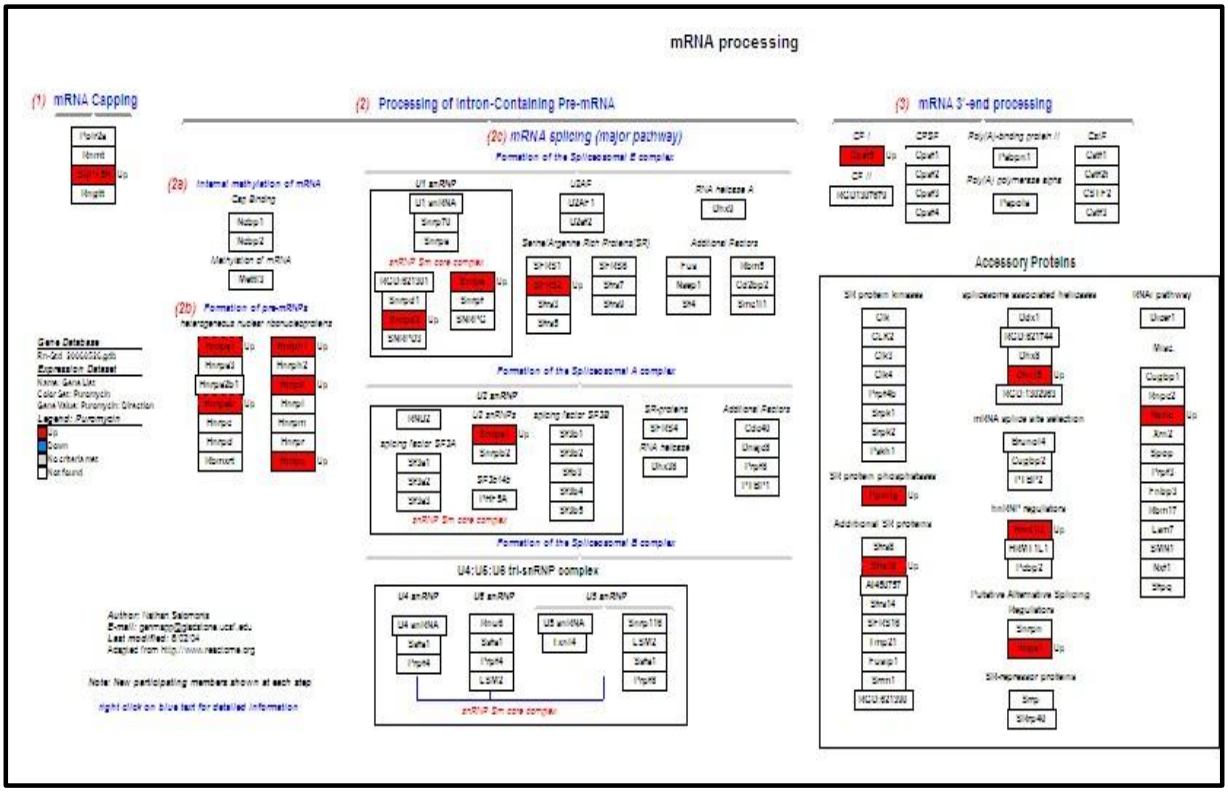

Figure 9: The expression profiles of the entire list of 1128 differentially expressed genes were used as input data in GenMAPP analysis.
All seventeen genes were up-regulated (red) in this pathway including six accessory proteins. Note that gene(s) from each step of mRNA processing are differentially expressed.

Pathway analysis also revealed that seven genes involved in protein translation were up-regulated after PUR treatment (Figure 10). These include Eif3s5 (eukaryotic translation initiation factor 3 subunit 5), Eif2b3 (eukaryotic translation initiation factor 2B subunit 3

gamma), Eifs1 (eukaryotic translation initiation factor 2 subunit 3 gamma), Eif4e (eukaryotic translation initiation factor 4E), Pabpc1 (poly(A) binding protein, cytoplasmic 1), Eef1b2 (eukaryotic elongation factor 1 beta 2), and Eef1g (eukaryotic elongation factor 1 gamma).

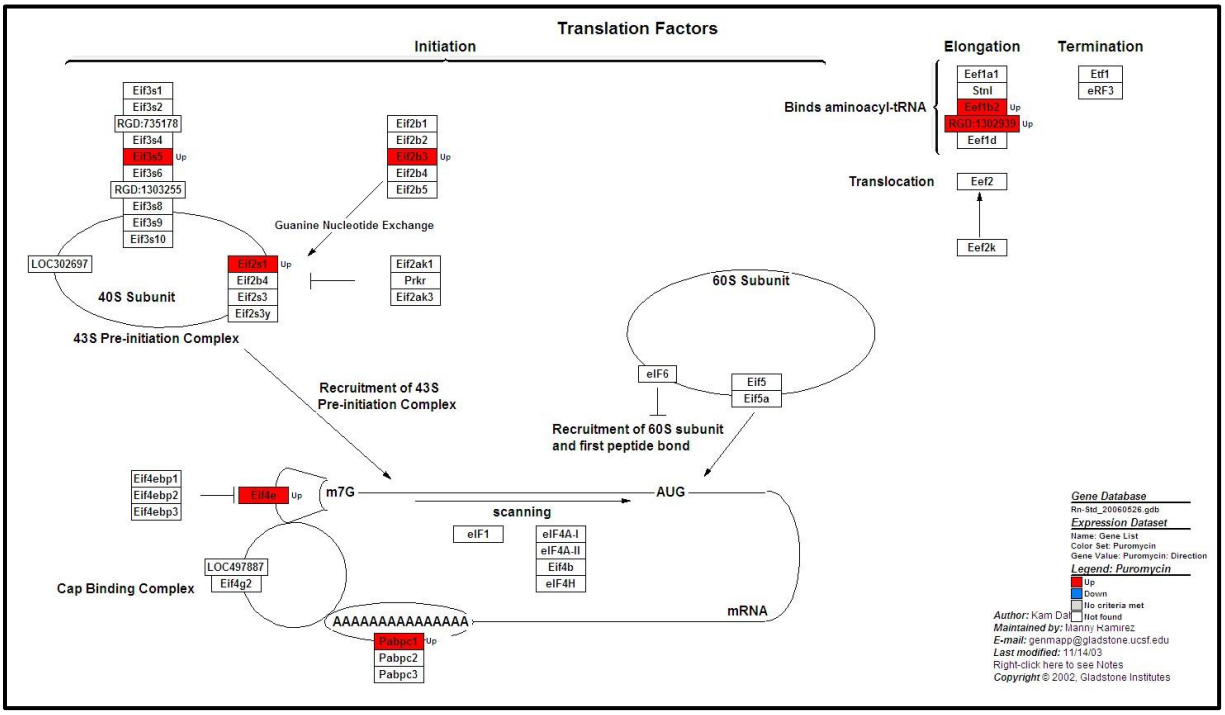

Figure 10: Gene Expression Changes Involved in Protein Translation
Pathway analysis was performed as described in Figure 7. Note that all seven genes are up-regulated (red).

Interestingly, eighteen genes involved in the calcium regulation of cardiac cells were differentially expressed following PUR treatment. Of the genes, fourteen were up-regulated, while four genes were down-regulated. The up-regulated genes include Fkbp1a (FK506 binding protein 1a), Atp2b1 (ATPase, Ca^{2+} transporting, plasma membrane 1), Prkar1a (protein kinase, cAMP dependent regulatory, type I, alpha), Camk2d (Ca^{2+}/calmodulin-dependent protein kinase II, delta), Calm1 (calmodulin 1), Calm2 (calmodulin 2), Gnb1 (guanine nucleotide binding protein, beta 1), Gnb2 (guanine nucleotide binding protein, beta polypeptide 2), Ywhab (tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide), Ywhah (tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide), Sfn (stratifin), Ywhaq (tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide), and Ywhaz (tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide). The down-regulated genes include Fxyd2 (FXYD domain-containing ion transport regulator 2), ATPase, Atp2a2 (Ca^{2+} transporting, cardiac muscle, slow twitch 2), Gng7 (guanine nucleotide binding protein, gamma 7), and Pkig (protein kinase inhibitor, gamma) (Figure 11).

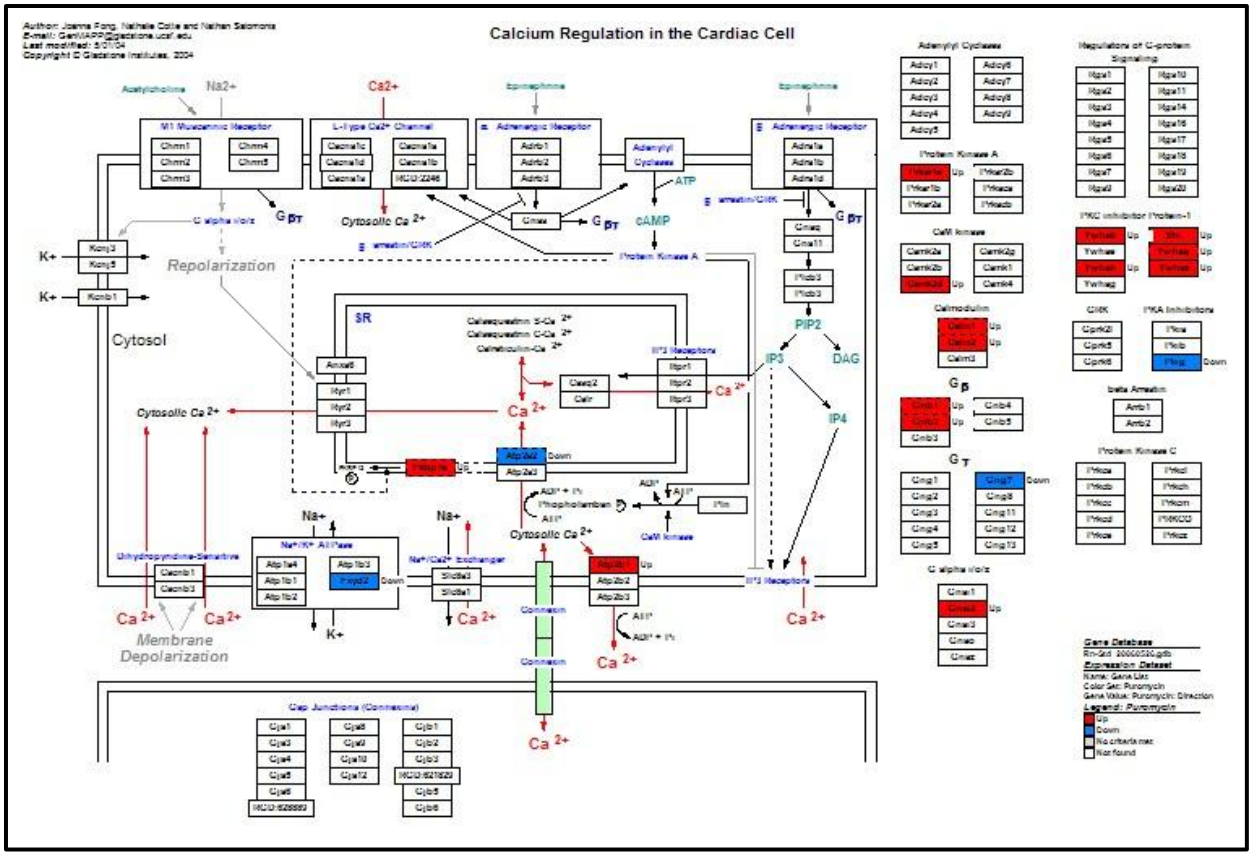

Figure 11: Gene Expression Changes Involved in Calcium Regulation in the Cardiac Cell
Pathway analysis was performed as described in Figure 7. In this pathway, 14 genes were up-regulated (red), while 4 genes were down-regulated (blue) after puromycin treatment.

3.3.4. AMPB Treatment

There were no significant gene expression changes in the kidney at 168 hr after AMPB treatment. This was most likely due to the formation of deposits of AMPB on the outside of the kidney as noted in the histopathologic analysis described above. No biological interpretation of this result was performed because of the negative differential gene expression outcome.

4. DISCUSSION

4.1. HPA Treatment

In this study, we investigated gene expression changes in the kidney 96 hr after HPA exposure. Although traditional techniques such as serum chemistry and histologic analyses showed no renal injury, a total of 206 genes, represented by 212 probe sets, were found to be differentially expressed after HPA treatment. CREA and BUN have been used extensively as clinical indices of changes in GFR to assess renal function. However, it is well known that the GFR has to decrease by more than 50% of its normal value before there are significant elevations of CREA and BUN (Vaamonde, 1986). In this study, serum chemistry analysis showed that

HPA treatment, even at the highest dose, failed to induce significant changes in CREA and BUN 96 hr after exposure, suggesting that there was no dramatic damage of the kidney functions at that time point. Although the exact reason(s) for this is not clear, it might be due to the fact that the doses of HPA used in this study failed to induce detectable toxic effect *in vivo* using traditional techniques. Alternatively, HPA treatment could indeed have resulted in significant cellular damage. However, these HPA-induced damages might have been repaired by the time the animals were scarified, and the kidney samples collected for DNA microarray analysis. Similar to the result of serum chemistry, histopathologic analysis showed no evidence of renal injury. In the absence of phenotypic changes, the interpretation of the biological consequences of HPA exposure solely based on gene expression changes can be challenging. However, despite this uncertainty, it is widely accepted that molecular end points, such as changes in gene expression, are much more sensitive than traditional end points like serum chemistry and histopathologic findings. Therefore, it is conceivable that the results described in this report represent authentic biological response to HPA exposure prior to the onset of renal injury observable using traditional techniques.

SOM clustering analysis indicates that the differentially expressed genes can be divided into two clusters that both show down-regulation after HPA treatment, but have distinct dose response patterns in terms of gene expression changes (see Figure 3). For instance, 38 genes represented in Cluster 1 show down-regulation even at the lowest dose of HPA and maintain a similar level throughout the entire dose range. On the other hand, 174 genes in Cluster 2 show little differential expression at low doses (0, 5, 50 and 500 mg/kg). However, as the dose increased to 750 – 1500 mg/kg, the expression of these genes was considerably down-regulated. Gene ontology analysis revealed that biological processes such as gene expression/transcription regulation and RNA metabolism are over-presented in Cluster 1, suggesting that these biological processes are highly sensitive to HPA treatment. Similarly, biological processes such as chromosome segregation/mitotic sister chromatid segregation and mRNA metabolism/transport are over-presented in Cluster 2, indicating that they are relatively resistant to low-dose HPA treatment. As the dose of HPA reaches 750 mg/kg or more, these biological processes were down-regulated. The implications of this finding is significant; down-regulation of gene expression, mRNA metabolism and mitotic cell replication will likely hinder the cellular defense and repair processes that meant to counter HPA toxicity and ultimately lead to compromised renal functions.

As differential expression of a large number of genes is observed, an efficient way to elucidate the biological implication of these expression changes is needed. To achieve this goal, a search of the NIAID DAVID databases was performed. Of the biological processes affected by the HPA treatment, the down-regulation of transcription regulation, mRNA processing, splicing and transport (see Table 7) are of particular interest. The cumulative effects of down regulation in these important pathways might be the cause of the overall gene repression after HPA treatment as observed in this study. Additionally, this analysis revealed a down-regulation of genes involved in cell cycle progression and mitotic sister chromatid segregation. Although the cause(s) of down-regulation of these pathways is not completely clear, suppression of the gene expression processes (i.e., down-regulation of transcription regulation, mRNA processing, splicing and transport) likely plays a significant role. It should be emphasized that cell cycle progression and mitotic sister chromatid segregation are fundamental to cell proliferation, which

is in turn essential for tissue repair/regeneration in response to toxic insults. Although over-representation of genes involved in apoptosis was not detected, this observation indeed suggests that HPA treatment can induce renal cell death. This notion is somewhat supported by the result of biological association network (see below).

Consistent with the result of gene ontology analysis, GenMAPP analysis also showed differential expression of genes involved in cell cycle control and mRNA processing/splicing among a large number of pathways affected by HPA treatment. In addition, down-regulation of pathways related to ion transports, including anion transport and metal ion transport (e.g. potassium transport) were also observed due to down-regulation of genes with ion channel activities such as Atp1b3-ATPase (Na+/K+ transporting, beta 3 polypeptide), Scnn1a (sodium channel, nonvoltage-gated, type I, alpha), Slc34a1 (solute carrier family 34 (sodium phosphate), member 1), Slc4a1 (solute carrier family 4 (anion exchanger), member 1), Slc4a3 (solute carrier family 4 (anion exchanger), member 3), Cacng3 (calcium channel, voltage-dependent, gamma subunit 3), Kcnc3 (potassium voltage gated channel, Shaw-related subfamily, member 3), and Kcnt1 (potassium channel, subfamily T, member 1) (Supplemental Data Table S3). Furthermore, Wnk4 (WNK lysine deficient protein kinase 4), which regulates the balance between NaCl reabsorption and K^+ secretion to maintain integrated homeostasis by regulating the membrane trafficking of the Na^+/Cl^- co-transporter (SLC12A3), was also down-regulated (Supplemental Data Table S1). As the primary role of the kidney is to maintain the homeostatic balance of bodily fluids by filtering and secreting metabolic end products (e.g. urea) and minerals from the blood, perturbation of these pathways would likely have significant impact on renal functions.

To gain further insights into the potential toxicity of HPA exposure, the differentially expressed genes were used as input data to construct a biological association network of all molecular interactions using PathwayArchitect. Since this tool allows the visualization of the interactions of these differentially expressed genes with their partners based on the mining of the scientific literature, it can potentially provide information that cannot be revealed by gene ontology and pathway analyses. There are 44 gene/protein nodes, three cellular process nodes and one small molecule node in the resultant network map. With the exception of one gene, Scnn1a, all differentially expressed genes captured in this network showed down-regulation after HPA treatment. This is consistent with the general phenomenon of HPA-induced gene repression as observed in the SOM clustering analysis. Close examination of the network map revealed that the two most highly connected nodes, Hnf4 and Taf1, are both members of the transcription factor family. While they showed no differential expression after HPA treatment, all the genes/proteins connected to them were down-regulated. As the primary mechanism of regulating transcription factor activity is post-translational modification and complex formation, this observation is not unexpected. This finding also suggested that the activities and/or levels of HNF4 and Taf1 might be down-regulated after HPA treatment at the level other than transcript level. Interestingly, two highly connected genes that showed down-regulation after HPA treatment, Hnrnpa1 and Sfrs2, are both involved in pre-mRNA processing (i.e., metabolism, splicing and transport) and connected to genes with no expression changes after HPA exposure. Despite this, the protein products of the genes connected to Hnrnpa1 and Sfrs2 are likely down-regulated, as the processing/splicing of their transcripts will be affected due to the down-regulation of Hnrnpa1 and Sfrs2. Interestingly, both Hnrnpa1 and Sfrs2 are connected to the

apoptotic process. As shown in this network map, apoptosis is connected to eleven HPA-induced down-regulated genes. Therefore, it is plausible that HPA treatment may have some impact on apoptosis, especially via novel apoptotic pathways, which may be the reason why activation of apoptosis was not observed in the gene ontology and pathway analyses.

4.2. D-Serine Treatment

We also examined gene expression changes in the kidney at 96 h after D-serine exposure in rats. A total of 1907 genes were found to be differentially expressed using a relatively stringent criterion that only the genes meeting the significance threshold of two statistical tests were included in the final gene list. This statistical procedure both narrowed the list of genes selected as differentially expressed, and leveraged the depth of across dose comparisions. SOM clustering analysis indicates that all the 1158 up-regulated genes show a homogenous dose-response profile (Cluster 1 of Figure 5). This was also observed with the down-regulated genes (Cluster 4 of Figure 5*)*. The reason for such homogenous dose response to D-serine in terms of gene expression changes is currently unknown. The result of this analysis also shows that a significant degree of gene expression changes only occurred in the high-dose groups (200 and 500 mg/kg). Although lower doses mainly induced smaller levels of changes (i.e. a fold change of $\sim$1.3 on average), differential expression of 153 genes did reach the statistical significance threshold used in these analyses.

The kidney functions to clear the body of metabolic end products while reabsorbing water and electrolytes for maintaining whole body homeostasis. Toxicants can affect renal tubular and vascular components producing decrements in homeostatic maintenance and endocrine functions of the kidney (Tarloff and Lash, 2005). In this study, clinical chemistry analysis showed significant increases in the levels of CREA and BUN within the 200 and 500 mg/kg treatment groups (see Table 3) suggesting the occurrence of significant damage of the kidney. This result is consistent with previously reported findings (Williams et al., 2003).

Histopathology analysis showed moderate nephropathy and tubular eosinophilic fluid leakage (Table 1), indicating damage of the kidney tubules, which is the portion of the kidney containing the fluid filtered through the glomerulus. A variety of kidney diseases are characterized by excessive deposition of glomerular matrix and elevated proliferation of glomerular mesangial cells (Floege et al., 1991). The proliferation of mesangial cells is associated with the remodeling process that occurs after kidney injury (Pichler et al., 1996). An important protein involved in tissue remodeling is SPARC (secreted protein acidic and rich in cysteine), which regulates the expression of a number of secreted proteins and matrix metalloproteinase's and is produced at sites of wound repair and tissue remodeling (Francki et al., 1999). Our result showed a strong up-regulation of the SPARC gene (see Supplemental Data Table S4), a finding that is consistent with the occurrence of significant renal damage. Therefore, DNA microarray analysis combined with standard clinical chemistry and histopathology analyses provides an opportunity to deeply survey and mechanistically assess D-serine nephrotoxicity.

As the number of genes underwent significant expression changes approached the two-thousand mark, an efficient way to elucidate the biological implication of these gene expression

changes was required. To achieve this goal, a search of the NIAID DAVID databases was performed. Of the biological processes activated following D-serine treatment, the up-regulation of the gene expression process (transcription initiation, mRNA processing/splicing and cytoplasmic ribosomal assembly, and translation elongation/initiation) is of particular interest. However, this is not unexpected as cell proliferation is actively in progress, as evidenced by the up-regulation of cell cycle regulation pathway involving G1-S transition. Although an apoptosis inhibitor for cell survival was up-regulated, a large number of genes promoting apoptosis were also up-regulated (see Table 11). The collective result of this expression pattern is likely to be pro-apoptotic. At this point, it is not clear whether the genes for cell proliferation and apoptosis were expressed in the same cell population, or were expressed in different populations. Considering that the kidney tissues were obtained at 96 h after D-serine exposure, the latter would be more likely in that the damaged cell population, which is being cleared by apoptosis, while renal regeneration is occurring simultaneously. At the same time, a portion of the damaged cells appeared to be also undergoing active repair of their protein and DNA contents as indicated by the activation of the proteasome pathway and the DNA repair pathway, respectively. The up-regulation of genes involved in stabilization of the actin cytoskeleton, G protein and calcium-mediated signaling pathways might play essential roles in these processes. On the other hand, the up-regulation of cell adhesion, metalloproteinase inhibitor precursors and major components of extracellular matrix suggests the activation of the fibrogenic pathway mediated by TGF-β pathway (see below).

As part of the differential gene expression in response to D-serine, a large number of metabolic pathways including fatty acid metabolism (mitochondrial fatty acid beta-oxidation), carbohydrate metabolism, amino acid metabolism, electron transport chain, TCA cycle, and ATP synthesis were down-regulated. This finding is consistent with that of Williams *et al* which showed a 60-70% decline in the ATP level was observed in the kidney within 4 h after D-serine treatment when necrosis of tubular epithelia first becomes evident (Williams et al., 2003). Taken together, these observations indicate that mitochondria are major targets of D-serine nephrotoxicity. Since tubular epithelia have strong energy demands for normal function, this result strongly suggests that disruption and impairment of energy metabolism may be mechanistically linked to D-serine-induced nephrotoxicity. Our gene expression results indicate that decreased energy metabolism persists even 96 h after a single-dose D-serine treatment. Considering a significant portion of these cell populations are under active regeneration and repair, down-regulation of these pathways will likely have a devastating effects on the success of the repair processes or mounting a defense against cytotoxic sequelae. Down-regulation of the pathways related to oxidative stress response, including antioxidant genes induction and glutathione metabolism, may also be related to the mechanism of D-serine-induced renal injury. Although the role of oxidative stress in D-serine nephrotoxicity is still not completely clear, D-serine exposure results in a 70% decline in the glutathione level (Krug et al., 2007). Consistent with this finding, our results show that glutathione metabolism is among the down-regulated pathways, which provides the mechanistic basis for the loss of cellular glutathione content as reported by Krug et al., (2007). Importantly, down-regulation of this pathway occurred even after low-dose D-serine treatment that produced no detectable lesions using traditional techniques such as clinical chemistry and histopathology. This observation may have important implications in D-serine nephrotoxicity, since glutathione production pathway could be considered as a first-line defense against oxidative stress, a common toxicological mechanism leading to cell death.

As the metabolism of D-serine by D-AAO in the peroxisomes of the tubular epithelial cells results in the generation of hydrogen peroxide - a reactive oxygen species (Silbernagl et al., 1999; Pilone, 2000), down-regulation of oxidative stress response pathways will likely exacerbate cellular injury and potentiate D-serine nephrotoxicity. Comparison of the dose effects of D-serine treatment on the perturbation of biological processes/pathways revealed another interesting finding. While most of the up-regulated pathways were not significantly affected by low-dose D-serine treatments (i.e. 5 – 50 mg/kg), in contrast, most of the down-regulated pathways, especially the glutathione metabolism pathway and those related to energy metabolism were significantly affected (see Table 11). This result further supports the notion that the down-regulation of energy metabolism and glutathione metabolism are relevant events in the mechanism of D-serine nephrotoxicity.

Consistent with previous findings concerning renal injury reported in the literature (Border and Noble, 1994; Peters et al., 1998), strong up-regulation of the TGF-β pathway was observed. TGF-β has been shown to be a key factor in renal injury due to glomerulosclerosis, interstitial fibrosis, or tubular atrophy. TGF-β can directly stimulate the synthesis of ECM components, inhibiting its degradation by reducing collagenase production, increasing integrin expression on cells to enhance matrix deposition (Peters et al., 1998), or indirectly inducing profibrogenic factors such as connective tissue growth factor resulting in fibrotics diseases characterized by the abnormal accumulation of ECM. The up-regulation of integrin-mediated cell adhesion molecules and ECM proteins (including collagens, laminins, fibronectin, biglycan, and tenascins, and tissue inhibitor of metalloproteinase 1 and 2) and the down-regulation of matrix metalloproteinase 1a (interstitial collagenase) observed in this study (for details see Supplemental Data Table S4) are consistent with this model.

Although several factors induce TGF-β expression in the kidney, one very interesting aspect is the link between the renin-angiotensin-aldosterone system (RAAS) and TGF-β. The ACE pathway is one of the most important regulators of the TGF-β pathway. ACE converts angiotensin I to angiotensin II (Brewster and Perazella, 2004), and overproduction of TGF-β in the kidney is induced by angiotensin II, or triggered by the excessive protein infiltration (Wolf et al., 1993). Additionally, angiotensin II up-regulates receptors for TGF-β. Angiotensin II perpetuates the production of nephritic reactive oxygen species and stimulates cell proliferation and tissue remodeling by enhancing the synthesis of profibrotic cytokines and growth factors (Wolf, 2000). As the onset of D-serine induced renal injury occurs within hours, the activation of the ACE pathway is expected to be an early event. However, our result showed that the ACE pathway is down-regulated in the kidney at 96 h after the D-serine treatment. Thus, it is possible that this pathway was up-regulated soon after D-serine treatment and subsequently down-regulated during renal regeneration at the later time point. Another explanation for the observed down-regulation of the ACE pathway could be due to severe damage caused by the treatment and a significant loss of epithelial cells of the proximal tubules. Previous studies have shown that renal proximal tubules have the highest ACE concentration in the kidney (Metzger et al., 1999).

It is well known that the mechanisms underlying renal fibrosis are complex and include a combination of several processes including cytokines that promote growth and enhance the release of ECM proteins. In normal kidney tissue, remodeling and turnover of the matrix proteins are balanced by metalloproteinases and their inhibitors (Sampson et al., 2001). In

fibrotic tissue, increased levels of matrix metalloproteinases inhibitors are observed, resulting in decreased degradation of the existing ECM, increased synthesis of ECM components and matrix accumulation in the tubulointerstitium (Sampson et al., 2001). Matrix degradation involves several enzyme systems, among the most important are the matrix metalloproteinases (MMP) (Docherty et al., 1992). One of these is MMP-2 that has been shown to be responsible for the EMC degradation of mesangial cells *in vitro* (Creely et al., 1992). In this study, MMP-2 was found to be significantly up-regulated. In addition to gene expression for the matrix proteins, expression levels of other immune response genes were also affected. Tissue damage is normally associated with an inflammatory response that results in macrophage infiltration (Sampson et al., 2001). Macrophages produce TGF-β, which is known to not only play a role in the development of fibrosis by stimulating matrix protein synthesis, but also to prevent matrix degradation by increasing production of metalloproteinases inhibitors (TIMP) (Creely et al., 1992; Edwards et al., 1987). In this study, an increase in gene expression of TIMP-1, TIMP-2, TGF-β and a large number of ECM components was observed, suggesting that high-level D-serine treatment caused significant damage to the kidney, which in turn triggers a cascade of events that lead to ECM accumulation and perhaps eventually leading to full-blown renal fibrosis. However, it should be emphasized that despite these gene expression changes, histopathological analysis revealed no evidence of tubulointerstitial fibrosis to any significant extent at the time period tested, although thickening of tubular basement membranes was noted. These results may seem contradictory. However, it has been reported that up-regulation of genes encoding ECM components precedes and predicts the accumulation of ECM and renal fibrosis in several experimental and clinical renal disorders (He et al., 1995; van Vliet et al., 1999; Eikmans et al., 2003; Baelde et al., 2004; Koop et al., 2004). Because of the time difference between gene expression changes, protein accumulation, and the onset of fibrotic lesion, the gene expression pattern as revealed in this study therefore strongly suggests the activation of the fibrogenic pathway following D-serine-induced tubular epithelia necrosis. The strong up-regulation (i.e. >14-fold) of vimentin, a marker of epithelial–mesenchymal transdifferentiation (Chai et al., 2003), further supports this notion.

DNA microarray analysis generates an enormous amount of data concerning gene expression changes resulting from chemical exposures. However, the biological relevance of these global gene expression changes or changes at the functional level must be defined. Our PathwayArchitect analyses showed a total of 275 up-regulated and 119 down-regulated genes in six different interaction networks (see Table 13) and each network is able to capture how different pathways might be coordinated at the level of promoter binding, protein post-translation modifications, protein complex formation, etc. thereby providing further insights into the plausible mechanism of D-serine toxicity. For instance, the regulation of the expression of ECM components and the regulation of the turnover of these proteins by MMPs and TIMPs are captured in the regulation network. It has been suggested that perturbation of the ECM contributes to tubular cellular proliferation and atrophy in renal diseases (Lewis et al., 1996) and that the components of the basement membrane such as laminin and collagen IV can modulate signaling events between epithelial cells and fibroblasts. Qualitative and quantitative changes in the basement membrane contribute to pathological changes in the tubulointerstitium, in part, by altering the function of tubular epithelia (Lewis et al., 1996, Nath, 1992). MMP2 is a proteolytic enzyme that degrades components of the basement membrane including laminin, collagen IV, and fibronectin (Romanic et al., 1994). Degraded products of these ECM components can

stimulate proliferation of epithelial cells for replacement of parenchyma or might eventually lead to tissue atrophy (Drago et al., 1991). It has also been demonstrated that disruption of epithelial cell-matrix interactions induces apoptosis (Frisch and Francis, 1994). It is of interest to note that the connection between the regulation of ECM synthesis and degradation involving the ECM components, MMPs and TIMPs and the apoptotic pathway which involves TNFRSF1A, IER3, MCL1, Stat3, P53, Myc, Casp3 and Casp8 is captured in the regulation network of our biological association network analysis. Our study also demonstrated changes in the expression of genes that produce cytokines such as interleukin 1 and TGF-β, which in turn promote growth of mesangial cells and enhance the expression of extracellular matrix proteins such as laminins, collagens, fibronectin and tenascins.

However, analyzing the kidney tissues at 96 h post-dosing will likely miss some early-stage gene expression changes. In light of this, it has been reported that rats treated 500 mg/kg D-serine have largely recovered at this time point and the levels of urinary protein and glucose have returned to control levels (Williams et al., 2003). In addition, the metabolic trajectory as revealed by principal component analysis of the urine NMR metabonomic data shows return to control values, except for the increased excretion of acetate and slight changes in citrate, lactate and alanine levels (Williams et al., 2003). However, our clinical chemistry and histopathological results showed maximal level of BUN at 96 h in animals treated with 500 mg/kg D-serine and persistent nephropathy of cortical and medullary tubular ectasia and intratubular eosinophilic protein fluid. The difference between our results and that of Williams may be due to differential sensitivity to D-serine toxicity of different strains of rats. In addition, performing gene expression profiling at a single time point fails to provide deep insights into the molecular events associated with the kinetics chemical-induced pre-injury changes and injury, as well as the subsequent repair process. The gene expression profiles identified in this study may represent a mixed pattern of toxic response, apoptosis, repair process, and tissue regeneration. However, due to the fact that the dynamics and kinetics of cellular response highly depends on the nature of the insult, as well as the magnitude of the insult, it is inevitable that at least some of the most significant gene expression changes in the major regulators associated with and/or essential for phase transition will be missed regardless the experimental design. Despite these limitations, activation of TGF-β signaling pathway, up-regulation of ECM components, inflammatory response, cell cycle regulation, and down-regulation of oxidative stress response and several major metabolic pathways, especially those related to energy metabolism, persist even 96 hr after a single D-serine treatment. Comparison of pathway perturbation between low- and high-dose treatments also revealed the selective sensitivity of glutathione and various energy metabolic pathways to low-dose D-serine exposure. Therefore, detailed biological interpretation of gene expression changes as presented here is able to provide interesting insights into the molecular basis of D-serine nephrotoxicity, and the cellular response subsequent to tubular epithelia necrosis.

In summary, DNA microarray technique was used to investigate the global gene expression changes in the kidney after D-serine exposure. Pathway analysis of the concomitant gene expression changes revealed the down-regulation of major metabolic pathways and oxidative stress response, while pathways related to tissue damage, repair and remodeling are up-regulated/activated. As demonstrated in this study, biological interpretation using advanced bioinformatics tools to reduce the complexity of DNA microarray result and select the most

significant feature groups in term of biological processes/pathways is essential for understanding the biological significance of differential expression of a large number of genes.

4.3. PUR Treatment

In this study, gene expression changes in the kidney following PUR treatment were examined in rats, and the expression levels of 1125 genes were found to be significantly altered after the treatment. As a relatively large number of differentially expressed genes were identified, the biological implications of these gene expression changes in the context of renal dysfunctions and/or injury were investigated.

CREA has been a commonly used indicator of renal function, but it lacks the sensitivity for detecting early-stage or low-level renal dysfunction. Consistent with this, mild lesions and mitotic figures suggestive of tissue regeneration were observed in histopathologic analysis of the kidney tissues from the animals treated with 150 mg/kg of PUR on day 7 post-dosing, while clinical chemistry showed no significant changes in CREA. Our result is consistent with that of Cutler et al., (1999) that no significant changes in CREA concentrations were observed in rats treated with a single dose of 100 mg/kg PUR up to 672 hours after treatment. Despite that CREA showed no changes in rats treated with PUR, the levels of BUN were significantly increased in the animals of the high-dose groups compared with the control and the low-dose groups. Although impaired renal function can cause an elevated level of BUN (Vaamonde, 1986), a small increase in BUN in the setting of a relatively normal creatinine as observed here, may be related to other pathophysiological conditions that occurred after PUR treatment such as excessive urea production, dehydration, shock, decrease of blood flow to the kidney, etc., rather than severe renal dysfunction.

Decreased TP levels were observed in the animals of the 75 & 150 mg/kg PUR treatment groups 24 hours post-dosing when compared to control and the low-dose treatment groups (see Table 4). A similar finding has been previously observed in PUR-induced nephrotic syndrome (Pedraza-Chaverrí et al., 1990; Pedraza-Chaverrí et al., 1993) that all major serum protein fractions (i.e. albumin, α1-globulin, α2-globulin, β-globulin and γ-globulin) were excreted in the urine of nephrotic rats. On the other hand, serum profiles of these protein fractions showed discordant changes (e.g. albumin and β-globulin were decreased; α1-globulin was increased; α2-globulin was unchanged; and γ-globulin was completely diminished) (Pedraza-Chaverrí et al., 1993). Since puromycin inhibits protein synthesis, by inducing premature chain termination during translation, this observation suggests that PUR treatment may have differential effects on the regulation, especially the synthesis of these proteins.

Histopathologic analysis revealed kidney lesions characterized by eosinophilic, hyaline protein casts multifocally within mildly dilated tubules (see Table 2). A similar observation of convoluted tubule dilation at 168 hr after PUR treatment was also reported by Cutler et al. (1999). While these changes are suggestive of glomerular damage and/or tubule epithelial cell compromise, further analyses using more refined techniques are needed to confirm this conclusion. Additonally, mitotic figures in cells lining these tubules was observed (Table 2), which likely represented regeneration of damaged tubule epithelial cells. An important cell cycle protein involved in cell regeneration and repair is PCNA (proliferating cell nuclear antigen)

(Tarloff and Lash, 2005), which is an essential component for cell proliferation (Wood and Shivji, 1997). Consistent with the presence of mitotic figures, as revealed in the histopathologic analysis of the kidney tissues from the animals that received high-dose PUR treatment, the gene encoding PCNA was up-regulated in the gene expression profiling analysis (see below). This highlights the unique advantage of combining transcriptomic analysis with histopathologic analysis as these molecular endpoints will provide mechanistic insights into the changes detected by traditional techniques.

Enrichment of the genes involved in several biological processes and pathways among the differentially expressed genes was identified by searching the NIAID DAVID database (Table 14). Close examination of the results of this analysis revealed that these biological processes/pathways could be grouped into several broad categories based on their roles in the overall cellular functions. For instance, biological processes and pathways related to cellular metabolisms were significantly down-regulated. These included amino acid metabolism, lipid metabolism, carbohydrate metabolism, nucleotide metabolism, coenzyme metabolism, cofactor metabolism, hormone metabolism, and energy production. This pattern of gene repression might be the result of severe toxicity from PUR treatment. While this general cellular machinery is suppressed, the cellular protective response to counter PUR toxicity would likely be hindered, resulting in the exacerbation of PUR-induced injury. Alternatively, it may be related to the suppression of cellular functions that are non-essential for protection against PUR toxicity. For instance, several genes involved in gluconeogenesis were down-regulated, including G6pc (glucose-6-phosphatase catalytic), Fpb1 (fructose-1,6-biphosphatase 1), Pck1 (phosphoenolpyruvate carboxykinase 1) and Pc (pyruvate carboxylase).

In addition, biological processes and pathways related to the response to xenobiotic stimulus, xenobiotic metabolism and sulfur compound metabolism were also significantly down-regulated. Xenobiotic metabolism is the process by which an organism eliminates foreign compounds (such as pharmaceuticals) from its system. Generally xenobiotic metabolism consists of two phases of drug metabolizing enzymes (DMEs). Phase 1 (modification) consists primarily of cytochrome P450 (CYP) enzymes as well as aldehyde hydrogenases (ALDH) and aldo-keto reductases (AKR), while Phase 2 (conjugation) consists of multiple superfamilies of enzymes including, sulfotransferases (SULT), UDP-glucuronosyltransferases (UGT), DT-diaphorase or NAD(P)H:guinone oxidoreductase (NQO) or NAD(P)H:menadione reductase (NMO), epoxide hydrolases (EPH), glutathione S-transferases (GST), and *N*-acetyltransferases (NAT) (see Xu et al., 2005 and Shimada, 2006 for review). With the exception of three cytochrome P450 genes, DMEs were down-regulated after puromycin treatment (Table 14). While most research on the effect of DMEs has focused on the liver, there is some evidence that down-regulation of DMEs also occurs in the kidney after xenobiotic treatments (see Korashy et al., 2004 for review). Consistently, our study showed that a phase 1 DME, Cyp2c was down-regulated after PUR treatment. A similar observation has also been reproted by Hendriksen et al., (2007) that Cyp2c was down-regulated in the kidney after exposure to benzene, mercury, trichloroethylene, and mixtures of these chemicals. In this same study, Gstm3 was up-regulated in the kidney. This result was in contrast to our result that PUR treatment induced down-regulation of this gene. These results highlighted the unique patterns of gene expression changes in a chemical-specific manner. Besides Cyp2c, several other cytochrome P450 genes (including Cyp2c23, Cyp2d4v1 and Cyp4f1) were also down-regulated after PUR treatment. Although the

exact mechanism of PUR-induced down-regulation of Cyp genes is not completely known, an important transcription factor regulating Cyp2 gene family expression is Hnf4a (hepatocyte nuclear factor 4α) (see Pavek et al., 2008 for review). Our result of Hnf4a down-regulation in kidney after PUR treatment thus provides some mechanistic insights into the PUR-induced down-regulation of the Cyp gene families. In addition to the down-regulation of the Cyp gene families, our results also showed that a large number of phase I DMEs (ALDHs and AKRs) and a large number of phase II enzymes (UGTs and GST-related enzymes) were also down-regulated after PUR tretament. Such a gene repression pattern could significantly impact the xenobiotic metabolizing capability and result in increased sensitivity to subsequent/secondary chemical exposure and toxicity.

Conversely, biological processes and pathways related to protein biosynthesis were significantly up-regulated. This finding was not unexpected considering the mode of action of puromycin. Since PUR is a potent inhibitor of protein translation, up-regulation of these pathways might represent a cellular response attempting to restore protein synthesis. Alternatively, this could also be related to the cell proliferation associated with tissue repair/remodeling (see below). Regardless of either alternative, the energy required for protein translation is significant; a total energy expenditure of approximately four high-energy phosphate bonds is needed for the incorporation of each amino acid residue. Up-regulation of protein translation on one hand, while down-regulation of cellular metabolisms and energy production on the other hand could induce severe enegy shortage, resulting in a shutdown of the cellular machinary and/or cell death.

Interestingly, the ubiquitin proteosome pathway was also significantly up-regulated after PUR treatment. This observation might seem paradoxical, as the cells already encounter deficits in protein synthesis. Since PUR inhibits protein translation by premature chain termination, up-regulation of this pathway likely indicates active clearance of truncated protein products due to premature chain termination during translation. A similar result was reported by Kaniuk et al., (2007) that PUR treatment of pancreatic β cells INS1 832/13 resulted in ubiquitinated protein aggregates.

In addition to protein synthesis, pathways related to the transcription, processing, splicing and transport of RNA (mRNA) were also up-regulated after PUR treatment. As protein translation is an essential step in the the overall process of gene expression, PUR-induced protein inhibition might also result in the increased activities in multiple steps in the gene expression process, including RNA transcription, processing, splicing and transport. Similarly, we cannot rule out that this increase in transcription could also be related to the cell proliferation associated with tissue repair/remodeling.

As expected, up-regulation of biological processes and pathways related to apoptosis was observed after PUR treatment. Up-regulation of apoptosis could be due to PUR-induced inhibition of cellular metabolisms, energy production, protein synthesis, or a combination of these pathways. Additionally, the up-regulation of apoptosis could be partially atributed to a decrease in the negative regulation of apoptosis, such as insulin-like growth factor 1 (Igf1) that was down-regulated after PUR treatment. Igf1 is a powerful inhibitor of apoptosis (see Fürstenberger and Senn, 2002 for review), and it is capable of blocking puromycin-induced

apoptosis in breast cancer cells (Söderlund et al., 2004). However, incomplete clearance of defective ribosomal product might also play a role in the activation of apoptosis, since accumulation of defective ribosomal products can lead to increased expression of apoptotic genes. Interestingly, antiapoptotic pathways were also up-regulated at the same time, although the number of up-regulated genes involved in the apoptotic pathways is about twice as many as that involved in the antipoptotic pathways. As this point, it is not clear if these apoptotic and antiapoptotic genes were expressed in the same cell population, or they were expressed in distinct populations (e.g. ones that were damaged beyond repair and the others that were under active repair, respectively).

Up-regulation of biological processes and pathways related to immune and inflammatory response were observed after PUR treatment. An example is the classical complement pathway. The initiator of the complement pathway is C1q (complement component 1, subcomponent q), which has been proposed to have a role in the removal of apoptotic cells. In its absence, apoptotic cells would accumulate, resulting in injury of surrounding tissue (Botto, 1998; Taylor et al., 2000). Activation of the classical complement pathway, specifically C5b-9, has also been implicated in mediating glomerular injury, and massive proteinuria and tubulointerstitial injury was observed in rats treated PUR (Nomura et al., 1997). Activation of C5b-9 could induce up-regulation of endoplasmic reticulum (ER) stress proteins, Bip (heat shock protein 5) and Grp94 (tumor rejection antigen gp96), which could limit complement-mediated glomerular visceral epithelial cell (GEC) injury (see Bijian and Cybulsky, 2005 for review). However, no differential expression of these genes was observed in our study, despite that up-regulation of C7 (complement component 7), a component of the C5b-9 complex, was detected. The failure to detect activation of C5b-9 and its target genes might be related to the time point selected for gene expression profiling. As histopathologic analysis indicates the occurrence of cell proliferation and tissue repair, rather than ongoing injury in the kidney on Day 7 after PUR treatment, activation of C5b-9 and its target genes might have occurred at eariler time points during the peak of renal injury and cell death. Another major player of the complement pathway, C3 (complement component 3), which has a central role in activation of the complement system, was also up-regulated. Interestingly, up-regulation of its inhibitor, Crry (complement receptor related protein), was also observed (see Supplemental Data Table S8). This finding is consistent with the result of gene expresion and histopathologic analyses descrived above, since Crry has been shown to prevent injury in PUR-mediated nephrotic syndrome (Hori et al., 1999; He et al., 2005).

Gene ontology analysis using the entire gene list as input data revealed the perturbation of the NF-κB signaling cascade after PUR tretament. Recent studies showed that NF-κB (Nfkb1- nuclear factor of kappa light polypeptide gene enhancer in B-cells 1) was shown to contribute to the pathogenesis of glomerular mesagnial cells in rats with Thy-1 nephritis (Wang et al., 2008), and inhibition of NF-κB with dehydroxymethyl-epoxyquinomicin (DHMEQ) in rats with induced glomerulonephritis resulted in decreased proteinuria (Kosaka et al., 2008). Although histopathologic analysis failed to definitely demonstrate glomerular damage in our study, the perturbation of the NF-κB signaling pathway as identified in the microarray analysis strongly suggested the occurrence of glomerular damage and/or tubule epithelial cell compromise. This result highlights the superior sensitivity of molecular analysis over traditional histopathologic analysis.

Besides inhibition of protein translation, PUR can also induce reactive oxygen species (ROS) production. Recent reports have shown that PUR treatment significantly increased ROS production that correlates with an increase in apoptosis of podocytes (Rincon et al., 2004; Oba et al., 2008) and that injury of podocytes by PUR-induced ROS production resulted in DNA damage and up-regulation of cell cycle checkpoint molecules leading to cell cycle arrest (Marshall et al., 2006). Consistent with these observations, our gene ontology analysis results using the entire gene list as input data also revealed up-regulation of the oxidative stress response pathway as well as DNA damage and repair pathways, although the enrichment of genes in the latter pathways failed to reach the threshold of statistical significance. Although the mechanism of PUR-induced ROS production is not completely clear, Cyp2b1 (cytochrome P450, family 2, subfamily b, polypeptide 1) may play a significant role in this model of glomerular injury. This enzyme is exclusively localized in the rat glomeruli, and treatment with PUR resulted in the generation of H_2O_2 in the glomerular basement membrane with significant loss of Cyp2b1content (Liu et al., 2002). The kinetics of PUR-induced ROS production is rapid. Previous studies have reported that ROS levels increased eight-fold in glomeruli 15 min after PUR injection (Gwinner et al., 1997). It then declined to baseline level in 24 h and maintained this low level until a second rise with a 14-fold increase nine days after the PUR treatment (Gwinner et al., 1997). Interestingly, a predominant involvement of hydroxyl radical and hydrogen peroxide was observed in the initial increase in ROS after PUR treatment, while superoxide anion and hydroxyl radical were found to contribute to the second rise in ROS.

There is up-regulation of pathways related to DNA replication and packaging, the establishment of chromatin architecture, chromosome biogenesis and organization, actin cytoskeleton organization and biogenesis and cellular morphogenesis. Such a pattern of gene activation is likely associated with the process of cell growth and proliferation as identified in the gene ontology analysis, as well as the finding of the histopathologic analysis. However, PUR treatment can directly induce reorganization of actin cytoskeleton preceding overt proteinuria via the p38 MAPK signaling pathway (Koshikawa et al., 2005), and inhibition of p38 MAPK activation could completely suppress proteinuria. Since the gene expression profiling was performed on Day 7 in our study, the up-regulation of actin cytoskeleton organization and biogenesis pathways was thus likely the result of cell growth and proliferation (and/or repair).

Consistent with the onset of tissue repair and regeneration, as suggested by the result of histopathologic analysis, microarray data suggested up-regulation of biological processes and pathways related to wound healing, tissue repair and regeneration, angiogenesis and cell adhesion. The genes invloved in these pathways that were up-regulated after PUR treatment are matrix proteins, matrix metalloproteinases, proteinase inhibitors, adhesion molecules, and growth factors. For instance, adhresion molecule Icam-1 (intercellular adhesion molecule-1), Itga1 (integrin alpha 1) and Itgb1 (integrin beta 1) were observed in this study. Increased expression of these genes has also been detected in PUR-induced nephritis (Martín et al., 1997). Recently it was demonstrated that integrin $\alpha 1\beta 1$ is a crucial regulator of glomerular injury (Chen et al., 2007). Besides the adhesion molecules, 24 genes involved in the regulation of cell adhesion were also up-regulated after PUR treatment (see Supplemental Data Table S8).

4.4. AMPB Treatment

We also attempted to investigate renal differential gene expression following AMPB treatment. However, no statistically significant gene expression change was detected at 168 hr after the treatment. Although the exact cause of this negative result is not completely clear, suboptimal experimental design and/or procedure appears to be responsible for the failure of the study. In order to elucidate the molecular mechanism of renal injury induced by AMPB, the study has to be repeated with better experimental design and execution.

5. CONCLUSIONS

In summary, differential gene expression was investigated in the kidneys from rats that have been exposed to HPA, D-serine, PUR and AMPB, using DNA microarray technology. The biological implications of these differential gene expression patterns were subsequently investigated using advanced bioinformatics and system biology techniques, including gene ontology analysis and pathway analysis. Coupled with SOM clustering analysis, we were able to identify co-regulated gene clusters with unique dose response, as well co-regulated gene clusters involved in specific biological processes/pathways that correlate with phenotypic changes as revealed in the clinical chemistry and histopathology analyses. In addition, biological association network analysis was performed. The results of these analysis provided insights into the functional interactions of the differentially expressed genes with their potential partners of diverse nature such as gene promoters, proteins and small molecules. Interestingly, these chemical treatments, with the exception of AMPB, resulted in chemical-specific patterns of differential gene expression and pathway perturbation.

Collectively, the combined results of these bioinformatic analyses provide important insights into the molecular basis for the perturbation of cellular processes and pathways that will facilitate further understanding of the coordination of the cellular response to these toxic insults. It should, however, be emphasized that in order to fully understand the molecular mechanisms of the cellular response to the exposure of these compounds, detailed analysis of the temporal changes in the transcriptomic profile to a broad dose range might be needed. This will allow the identification of adaptive response from toxic response that ultimately lead to nephrotoxin-induced organ damage. As demonstrated in this study, a combined use of advanced biotechnologies such as DNA microarrays and bioinformatics can undoubtedly facilitate the identification of mechanism-based biomarkers for chemical exposure or other environmental stressors. If a large number of data sets consisting of chemicals with diverse target organ specificity were available, differential gene expression identified using an approach similar to that employed in this study could ultimately beome useful biomarkers for early detection and/or prediction of organ damage.

However we would like to emphasize that in analyzing DNA microarray data, the biological relevance of gene expression changes responsive to perturbations has to be evaluated in the context of phenotypic changes - adaptive response, toxic response, repair, apoptosis/necrosis, or regeneration. For example, induction of genes associated with DNA repair

itself represents an essential defense mechanism of the organism, but may also be a signal of the occurrence of DNA damage. If the damage is extensive, other pathways such as apoptosis may be activated to eliminate the damaged cell population that is beyond repair. A global view of changes in various cellular pathways as provided by pathway analysis of the DNA microarray data will facilitate the proper interpretation of the significance of these changes, which in turn will facilitate the assessment of cellular integrity and provide hypothesis for protein activity and content studies, as well as define fully the disturbance of homeostasis of cells and tissues.

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APPENDIX

AFFY_ID	Gene Name
1389396_at	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4
1370911_at	a kinase (prka) anchor protein 8
1385713_at	a kinase (prka) anchor protein 8-like
1388179_at	activin receptor iib
1367644_at	adenylate cyclase 6
1375577_at	adenylate kinase 3
1373619_at	ankyrin repeat domain 10
1389339_at	arylsulfatase a
1376523_at	at rich interactive domain 4a (rbp1 like) (predicted)
1377195_at	atpase, na+/k+ transporting, beta 3 polypeptide
1368452_at	atp-binding cassette, sub-family c (cftr/mrp), member 6
1387184_at	axin2
1374327_at	bardet-biedl syndrome 4 (predicted)
1373247_at	beta-site app cleaving enzyme
1373494_at	breakpoint cluster region (predicted)
1376533_at	bromodomain adjacent to zinc finger domain, 2b (predicted)
1372207_at	bromodomain containing 8
1372068_at	bs69 protein
1399141_at	cdc like kinase 4
1373893_at	cdc23 (cell division cycle 23, yeast, homolog)
1399022_at	cdc-like kinase 1
1375353_at	cdk5 and abl enzyme substrate 1 (predicted)
1375850_at, 1390100_s_at	chloride intracellular channel 1
1367718_at	choline kinase beta
1371672_at	chromobox homolog 7
1389137_at	citron
1398394_at	collagen, type xviii, alpha 1
1389564_at	cyclin l2
1399100_at	cyclin t2 (predicted)
1373682_at	dead (asp-glu-ala-asp) box polypeptide 51 (predicted)
1399123_at	dead/h (asp-glu-ala-asp/his) box polypeptide 26
1380371_at	delangin
1387190_at	diacylglycerol kinase, alpha (80 kda)
1369997_at	dishevelled, dsh homolog 1 (drosophila)
1388589_at	dot1-like, histone h3 methyltransferase (s. cerevisiae) (predicted)
1368292_at	dynamin 1
1368649_at	dyskeratosis congenita 1, dyskerin
1373915_at	dystrophia myotonica kinase, b15 (predicted)
1375728_at	ectonucleoside triphosphate diphosphohydrolase 4 (predicted)
1382952_at	elav (embryonic lethal, abnormal vision, drosophila)-like 1 (hu antigen r) (predicted)

Supplemental Data Table S1. Continued.

1374995_at	engulfment and cell motility 3, ced-12 homolog (c. elegans)
1371477_at	EST
1372911_at	EST
1373261_at	EST
1373403_at	EST
1374896_at	EST
1374963_s_at	EST
1375011_at	EST
1375308_at	EST
1376097_at	EST
1376301_at	EST
1376531_at	EST
1376840_at	EST
1377237_at	EST
1377531_at	EST
1379093_at	EST
1379511_at	EST
1383102_at	EST
1384868_at	EST
1386257_at	EST
1386376_at	EST
1389259_at	EST
1389392_at	EST
1389616_at	EST
1389774_at	EST
1389953_at	EST
1390206_at	EST
1391485_at	EST
1392778_at	EST
1389957_at	EST, highly similar to jw0059 mtprd protein - mouse (m.musculus)
1385438_at	EST, weakly similar to 810024j urf 4 (h.sapiens)
1376760_at	EST, weakly similar to a33633 transcription repressor protein gcf (h.sapiens)
1373260_at	est, weakly similar to cerl rat cerebellin-like glycoprotein (r.norvegicus)
1393739_at	EST, weakly similar to s21345 retrovirus-related leucine zipper protein p40 - rat retrotransposon (r.norvegicus)
1390300_at	EST, weakly similar to s21976 probable rna-directed dna polymerase (r.norvegicus)
1372823_at	family with sequence similarity 36, member a (predicted)
1388295_s_at	fibroblast growth factor receptor substrate 3
1368550_at	forkhead box q1
1376992_a_at	forkhead box r1 (predicted)
1374690_at	gle1 rna export mediator-like (yeast)
1386883_at	glycogen synthase kinase 3 alpha
1374706_at	growth differentiation factor 11
1377238_at	guanosine monophosphate reductase 2
1372693_at	heterogeneous nuclear ribonucleoprotein a1
1370969_at	homeo box a5
1370454_at	homer homolog 1 (drosophila)
1374294_at	hypothetical loc293513

Supplemental Data Table S1. Continued.

1372356_at	hypothetical protein
1372193_at	imprinted and ancient
1389176_at	inositol polyphosphate-5-phosphatase f (predicted)
1390671_at	insulin-like growth factor 1 receptor
1367921_at	integrin-linked kinase-associated serine/threonine phosphatase 2c
1371560_at	interferon regulatory factor 3
1389374_at	kinesin family member c3
1367880_at	laminin, beta 2
1367996_a_at	latrophilin 1
1392932_at	leukocyte receptor cluster (lrc) member 8
1389986_at	loc499304
1387959_at	lysophospholipase
1375392_at	meis1, myeloid ecotropic viral integration site 1 homolog 2 (predicted)
1375232_at	methyl-cpg binding domain protein 6 (predicted)
1376136_at	miro2 protein
1371042_at	mitogen-activated protein kinase kinase kinase kinase 3
1377208_at	muscleblind-like 2 (predicted)
1375573_at, 1375703_at	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, drosophila)
1387110_at	n-arginine dibasic convertase 1
1398861_at	nuclear RNA export factor 1
1375374_at	sequestosome 1 (oxidative stress induced)
1368303_at	period homolog 2 (drosophila)
1374632_at	phosphatidylserine receptor
1369222_at	potassium channel subunit (slack)
1369134_x_at	potassium voltage gated channel, shaw-related subfamily, member 3
1390305_at	protein kinase c binding protein 1
1389662_at	protein kinase, lysine deficient 4
1378124_at	protein phosphatase 1b, magnesium dependent, beta isoform
1376537_at	protein tyrosine phosphatase, non-receptor type 3
1389684_at	prp39 pre-mrna processing factor 39 homolog (yeast) (predicted)
1375396_at	pumilio 1 (drosophila) (predicted)
1372936_at	purkinje cell protein 2 (l7)
1376393_at	ral gef with ph domain and sh3 binding motif 2
1387209_at	regucalcin gene promotor region related protein
1374448_at	reversion-inducing-cysteine-rich protein with kazal motifs (predicted)
1390494_at	ribosomal protein s24
1371020_at	rim binding protein 2
1390047_at	rio kinase 3 (yeast) (predicted)
1377087_at	sec31-like 1 (s. cerevisiae)
1390048_at, 1398940_at	serine/arginine repetitive matrix 2 (predicted)
1375191_at	serine/threonine kinase 32c (predicted)
1387417_a_at	sh2-b ph domain containing signaling mediator 1
1374417_at	siah binding protein 1; fbp interacting repressor; pyrimidine tract binding splicing factor; ro ribonucleoprotein-binding protein 1
1374028_at	similar to cdna sequence bc024479
1398446_at	similar to chromosome 1 open reading frame 2 (predicted)
1398364_at	similar to chromosome 1 open reading frame 63

Supplemental Data Table S1. Continued.

1380883_at	similar to chromosome 13 open reading frame 3 (predicted)
1399018_at	similar to cisplatin resistance-associated overexpressed protein (predicted)
1389913_at	similar to fli-lrr associated protein-1
1373954_at	similar to flj00052 protein (predicted)
1374024_at	similar to glycoprotein iib - rat
1375141_at	similar to hox11l2
1373191_at	similar to hypothetical protein
1373407_at	similar to hypothetical protein 9930016o13 (predicted)
1372699_at	similar to hypothetical protein c130032f08 (predicted)
1390281_a_at	similar to hypothetical protein flj32452
1377793_at	similar to hypothetical protein mgc20460 (predicted)
1398425_at	similar to hypothetical protein mgc39325-like protein
1390261_at	similar to kiaa1089 protein (predicted)
1373782_a_at	similar to loc495800 protein
1372010_at	similar to mk-5 type 2
1376136_at	similar to mkiaa1924 protein
1374364_at	similar to mkiaa1931 protein
1372532_at	similar to m-rdgb2 retinal degeneration protein b subtype 2
1371817_at	similar to myo-inositol 1-phosphate synthase a1
1376175_at	similar to nipsnap2 protein (glioblastoma amplified sequence)
1390271_at	similar to pleckstrin homology domain containing, family a member 6
1376374_at	similar to polycystic kidney disease 2
1390518_at	similar to putative emu1 protein
1374170_at	similar to putative traf and TNF receptor associated protein
1376710_at	similar to pym protein
1390093_at	similar to ribulose-5-phosphate-3-epimerase
1376824_at	similar to riken cDNA 1700027m01
1373699_at	similar to riken cDNA 1810059a23
1373315_at	similar to riken cDNA 2210412d01
1390491_at	similar to riken cDNA 2310005o14
1376853_at	similar to riken cDNA 2310042p20
1373474_at	similar to riken cDNA 2810403a07
1388637_at	similar to riken cDNA 4632411b12
1385204_at	similar to riken cDNA 4833418a01
1390194_at	similar to riken cDNA 4933435a13
1376776_at	similar to riken cDNA 5330440m15
1374874_at	similar to riken cDNA 5730509k17 gene
1374159_at	similar to rn49018 (predicted)
1371838_at	similar to splicing factor, arginine/serine-rich 2
1373534_at, 1398440_at	similar to sr rich protein
1388964_at	similar to transcription factor (p38 interacting protein)
1389443_at	similar to ubiquinol-cytochrome c reductase complex 7.2 kda protein (cytochrome c1, nonheme 7 kda protein) (complex iii subunit x) (7.2 kda cytochrome c1-associated protein subunit) (hspc119)
1376366_at	snap-associated protein
1387104_at	sodium channel, nonvoltage-gated, type i, alpha polypeptide
1370610_at	solute carrier family 34 (sodium phosphate), member 1
1369634_at	solute carrier family 4, member 1

Supplemental Data Table S1. Continued.

1368772_at	solute carrier family 4, member 3
1370398_at	spermatogenesis associated 7
1389840_at	splicing factor 3b, subunit 1
1368992_a_at	splicing factor, arginine/serine-rich 5
1388658_at	surfeit 2
1377312_at	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2
1375469_at	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
1369628_at	synaptic vesicle glycoprotein 2b
1390540_at	syntaphilin (predicted)
1367530_at	syntaxin 16 (predicted)
1388473_at	tbc1 domain family, member 14
1372293_at	toll-like receptor 5
1373553_at	topoisomerase (dna) iii beta (predicted)
1373922_at	tpr domain, ankyrin-repeat and coiled-coil-containing
1390248_at	transcription factor pur-beta
1398401_at	tudor domain containing 3
1371742_at, 1390345_at	u1 small nuclear ribonucleoprotein polypeptide a (predicted)
1398436_at	ubiquitin specific protease 42 (predicted)
1389022_at	ubiquitin specific protease 52
1376954_at	upstream transcription factor 2
1373807_at	vascular endothelial growth factor a
1384169_a_at, 1393349_x_at	vav2 oncogene (predicted)
1368614_at, 1377013_at	williams-beuren syndrome chromosome region 14 homolog (human)
1374027_at	zinc finger protein 187
1374189_at	zinc finger protein 219
1376917_at	zinc finger protein 292
1368712_at	zinc finger protein 386 (kruppel-like)

Supplemental Data Table S2. Enriched Gene Ontology Categories Among HPA-Induced Renal Gene Expression Changes as Determined by DAVID Analysis.

Category	Term	Count	P-Value
GOTERM_BP_ALL	biopolymer metabolism	28	4.20E-02
GOTERM_BP_ALL	cellular physiological process	89	1.50E-02
GOTERM_BP_ALL	chromosome segregation	4	3.80E-03
GOTERM_BP_ALL	mitotic sister chromatid segregation	3	1.40E-02
GOTERM_BP_ALL	mRNA metabolism	9	2.10E-04
GOTERM_BP_ALL	mRNA processing	7	2.60E-03
SP_PIR_KEYWORDS	mRNA transport	3	3.50E-03
GOTERM_BP_ALL	nucleobase, nucleoside, nucleotide and nucleic acid metabolism	36	6.10E-04
GOTERM_BP_ALL	regulation of cell cycle	9	4.90E-02
GOTERM_BP_ALL	regulation of cellular metabolism	22	2.70E-02
GOTERM_BP_ALL	regulation of cellular physiological process	35	1.30E-02
GOTERM_BP_ALL	regulation of cellular process	36	2.70E-02
GOTERM_BP_ALL	regulation of metabolism	24	1.70E-02
GOTERM_BP_ALL	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolism	22	6.20E-03
GOTERM_BP_ALL	regulation of physiological process	36	2.60E-02
GOTERM_BP_ALL	regulation of progression through cell cycle	9	4.80E-02
GOTERM_BP_ALL	regulation of RNA metabolism	3	1.80E-02
GOTERM_BP_ALL	regulation of transcription	20	2.00E-02
GOTERM_BP_ALL	regulation of transcription, DNA-dependent	20	7.40E-03
GOTERM_BP_ALL	RNA metabolism	11	2.70E-03
GOTERM_BP_ALL	RNA processing	9	4.70E-03
GOTERM_BP_ALL	RNA splicing	5	3.50E-02
GOTERM_BP_ALL	sister chromatid segregation	3	1.40E-02
GOTERM_BP_ALL	transcription	21	2.50E-02
GOTERM_BP_ALL	transcription, DNA-dependent	20	1.60E-02
GOTERM_CC_ALL	intracellular membrane-bound organelle	45	3.70E-02
GOTERM_CC_ALL	membrane-bound organelle	45	3.90E-02
GOTERM_CC_ALL	nucleus	34	5.10E-04
INTERPRO_NAME	A-kinase anchoring protein 95 (AKAP95)	2	2.80E-02
SP_PIR_KEYWORDS	alternative splicing	14	2.30E-02
SP_PIR_KEYWORDS	anion exchange	2	3.90E-02
INTERPRO_NAME	Anion exchange protein	2	4.10E-02
SP_PIR_KEYWORDS	ATP-binding	12	2.50E-02
INTERPRO_NAME	BRK	2	2.80E-02
SMART_NAME	BROMO	6	7.10E-05
INTERPRO_NAME	Bromodomain	5	4.30E-06
INTERPRO_NAME	DIX	2	2.80E-02
UP_SEQ_FEATURE	domain:DIX	2	2.40E-02
GOTERM_MF_ALL	enzyme binding	7	2.40E-02
INTERPRO_NAME	HSA	2	2.80E-02
GOTERM_MF_ALL	inorganic anion transporter activity	3	5.00E-02
SP_PIR_KEYWORDS	kinase	13	2.00E-03
GOTERM_MF_ALL	kinase activity	15	1.40E-02

Supplemental Data Table S2. Continued.

SP_PIR_KEYWORDS	nuclear protein	18	2.70E-02
GOTERM_MF_ALL	nucleic acid binding	34	4.20E-04
SP_PIR_KEYWORDS	nucleotide-binding	14	4.00E-02
INTERPRO_NAME	Nucleotide-binding, alpha-beta plait	5	2.10E-02
SMART_NAME	PHD	4	3.40E-02
GOTERM_MF_ALL	phosphotransferase activity, alcohol group as acceptor	15	3.80E-03
GOTERM_MF_ALL	protein kinase activity	11	4.30E-02
GOTERM_MF_ALL	protein serine/threonine kinase activity	11	1.00E-02
GOTERM_MF_ALL	RNA binding	12	3.90E-03
INTERPRO_NAME	RNA-binding region RNP-1 (RNA recognition motif)	5	2.70E-02
INTERPRO_NAME	Serine/threonine protein kinase, active site	7	2.80E-02
SP_PIR_KEYWORDS	serine/threonine-protein kinase	7	2.20E-02
PIR_SUPERFAMILY_NAME	SF002468:band 3 anion transport protein	2	3.50E-02
INTERPRO_NAME	SNF2-related	2	2.80E-02
UP_SEQ_FEATURE	splice variant	13	9.30E-03
GOTERM_MF_ALL	transferase activity, transferring phosphorus-containing groups	15	3.60E-02
INTERPRO_NAME	Zinc finger, PHD-type	3	1.40E-02

Supplemental Data Table S3. Potential Perturbation of Pathways Resulting from HPA-Induced Renal Gene Expression Changes. The List of Pathways and the Direction of Expression Changes Involved in each of these Pathways under Various Categories Were Determined Based on GenMAPP Analysis.

Molecular Function				
Pathway	**Gene**	**Description**	**Function**	Change direction
ATPase activity, couples	Abcc6	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	human homolog acts as a Mg-ATP-dependent efflux pump that transports glutathione S-conjugates and mediates a low level of resistance to some anticancer agents	down
	Atp1b3	ATPase, Na+/K+ transporting, beta 3 polypeptide	plays a role in Na+ and K+ transport	down
ATPase activity	Abcc6	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	human homolog acts as a Mg-ATP-dependent efflux pump that transports glutathione S-conjugates and mediates a low level of resistance to some anticancer agents	down
	Atp1b3	ATPase, Na+/K+ transporting, beta 3 polypeptide	plays a role in Na+ and K+ transport	down
Binding	Nasp	nuclear autoantigenic sperm protein (histone-binding)		down
	RGD1308697	similar to hypothetical protein FLJ10579		down
Carbohydrate Binding	Vegfa	vascular endothelial growth factor A	This gene product is a member of the PDGF/VEGF growth factor family. It is a mitogen that specifically acts on endothelial cells and has various effects, including mediating increased vascular permeability, inducing angiogenesis, vasculogenesis, endothelial cell growth, promoting cell migration, and inhibiting apoptosis. Alternatively spliced transcript variants encoding different isoforms have been found for this gene. Also, alternative translation initiation from non-AUG (CUG) and AUG start sites in some transcript variants, give rise to additional isoforms.	down
	Lphn1	latrophilin 1	G protein-coupled receptor for alpha-Latrotoxin	down
	Cacng3	calcium channel, voltage-dependent, gamma subunit 3	member of a family of gamma subunits of voltage-dependent calcium channels	down

Supplemental Data Table S3. Continued.

Cation channel activity	Kcnt1	potassium channel, subfamily T, member 1	Na(+)-activated potassium channel; may be involved in regulating the firing properties of neurons	down
	Kcnc3	potassium voltage gated channel, Shaw-related subfamily, member 3	transient voltage-dependent potassium channel	down
	Scnn1a	sodium channel, nonvoltage-gated 1 alpha	acts as an epithelial sodium ion channel; regulates salt and fluid transport in the kidney	down
Electrochemical potential-driven transport activity	Slc4a3	solute carrier family 4, member 3	transmembrane anion transporter; functions as a chloride/bicarbonate exchanger; may be important for bicarbonate absorption in the heart	down
	Slc4a1	solute carrier family 4, member 1	a transporter; functions as a chloride/carbonate exchanger and binds to components of the cytoskeleton	down
	Slc4a3	solute carrier family 4, member 3	transmembrane anion transporter; functions as a chloride/bicarbonate exchanger; may be important for bicarbonate absorption in the heart	down
Magnesium ion binding	Dnm1	dynamin 1	mediates GTP hydrolysis; plays a role in receptor mediated endocytosis; required for agonist-induced internalization of the epidermal growth factor receptor	down
	Adcy6	adenylate cyclase 6	may play a role in intracellular signaling	down
	Ilkap	integrin-linked kinase-associated serine/threonine phosphatase 2C		down
	Ppm1b	protein phosphatase 1B, magnesium dependent, beta isoform		down
phospheric ester hydrolase activity	Ilkap	integrin-linked kinase-associated serine/threonine phosphatase 2C		down
	Ppm1b	protein phosphatase 1B, magnesium dependent, beta isoform		down
phosphric monoesterase hydrolase activity	Ilkap	integrin-linked kinase-associated serine/threonine phosphatase 2C		down
	Ppm1b	protein phosphatase 1B, magnesium dependent, beta isoform		down
porter activity	Slc4a1	solute carrier family 4, member 1	a transporter; functions as a chloride/carbonate exchanger and binds to components of the cytoskeleton	down
	Slc34a1	solute carrier family 34 (sodium phosphate), member 1	membrane carrier protein that may be involved with active transport of phosphate into cells via sodium cotransport	down

Supplemental Data Table S3. Continued.

potassium channel activity	Kcnt1	potassium channel, subfamily T,	Na(+)-activated potassium channel; may be involved in regulating the firing properties of neurons	down
	Kcnc3	potassium voltage gated channel, Shaw-related subfamily, member 3	transient voltage-dependent potassium channel	down
Protein serine/ threonin kinase activity	Clk4	CDC like kinase 4		down
	Cit	citron	a serine/threonine kinase; involved in regulating G2/M transition	down
	Wnk4	WNK lysine deficient protein kinase 4	mutation of the human homolog causes pseudohypoaldosteronism type II	down
	Clk1	CDC-like kinase 1		down
RNA binding	Nxf1	nuclear RNA export factor 1	mouse homolog is involved in nuclear export of RNA transcripts and associates with NXT1	down
	Sfrs5	splicing factor, arginine/serine-rich 5	may act as a regulator of alternative pre-mRNA splicing; may play a role in cell cycle regulation	down
	Pum_puf_RNA_bd	Pumilio/Puf RNA-binding		down
signal trasducer activity	Axin2	axin2	inhibits axis formation; acts as a negative regulator of the Wnt signaling pathway by inducing GSK-3beta-dependent phosphorylation of beta-catenin	down
	Dvl1	dishevelled, dsh homolog 1 (Drosophila)	mouse homolog contributes to social and sensorimotor behavior	down
	Per2	period homolog 2 (Drosophila)	may play a role in regulation of circadian rhythm and locomoter activity	down
voltage-gated ion channel activity	Cacng3	calcium channel, voltage-dependent, gamma subunit 3	member of a family of gamma subunits of voltage-dependent calcium channels	down
	Kcnc3	potassium voltage gated channel, Shaw-related subfamily, member 3	transient voltage-dependent potassium channel	down

Supplemental Data Table S3. Continued.

Cellular Process				
Pathway	**Gene**	**Description**	**Function**	**Change Direction**
Local adhesion	Lamb2	laminin, beta 2	a component of the basal lamina; may be involved in motor neuron function	down
	Vegfa	vascular endothelial growth factor A	This gene product is a member of the PDGF/VEGF growth factor family. It is a mitogen that specifically acts on endothelial cells and has various effects, including mediating increased vascular permeability, inducing angiogenesis, vasculogenesis, endothelial cell growth, promoting cell migration, and inhibiting apoptosis. Alternatively spliced transcript variants encoding different isoforms have been found for this gene. Also, alternative translation initiation from non-AUG (CUG) and AUG start sites in some transcript variants, give rise to additional isoforms.	down
	Igf1r	insulin-like growth factor 1 receptor	receptor for Igf-1; involved in induction of cell cycle progression and survival in many cell types	down
IL-3_netPath_15	Dnm1	dynamin 1	mediates GTP hydrolysis; plays a role in receptor mediated endocytosis; required for agonist-induced internalization of the epidermal growth factor receptor	down
	Gsk3a	glycogen synthase kinase 3 alpha	protein-serine kinase; may mediate hormonal control of several regulatory proteins including glycogen synthase and the transcription factor c-jun	down
Insulin Signaling	Gsk3a	glycogen synthase kinase 3 alpha	see the above	down
	Map4k3	mitogen-activated protein kinase kinase kinase kinase 3	a mitogen-activated protein kinase kinase kinase kinase that functions upstream of c-Jun N-terminal kinase	down
Mark Signaling	Map4k3	mitogen-activated protein kinase kinase kinase kinase 3	a mitogen-activated protein kinase kinase kinase kinase that functions upstream of c-Jun N-terminal kinase	down
	Ppm1b	protein phosphatase 1B, magnesium dependent, beta isoform		down

Supplemental Data Table S3. Continued.

mRNA_processing_Reactome	Hnrpa1	heterogeneous nuclear ribonucleoprotein A1	involved in the packaging of pre-mRNA into heterologous nuclear ribonucleoprotein particles and in the transport of poly-A mRNA from the nucleus to the cytoplasm; may modulate splice site selection	down
	Snrp70_predicted	U1 small nuclear ribonucleoprotein polypeptide A (predicted)	no listing	down
	Sfrs2	similar to splicing factor, arginine/serine-rich 2	no listing	down
	Sfrs5	splicing factor, arginine/serine-rich 5	no listing	down
	Sf3b1	splicing factor 3b, subunit 1	mouse homolog is a subunit of the U2 snRNP that is necessary for prespliceosome assembly and splicing catalysis	down
	Clk4	CDC like kinase 4		down
	Nxf1	nuclear RNA export factor 1	mouse homolog is involved in nuclear export of RNA transcripts and associates with NXT1	down
TGF-beta-Receptor_netPath	Axin2	Axin2	inhibits axis formation; acts as a negative regulator of the Wnt signaling pathway by inducing GSK-3beta-dependent phosphorylation of beta-catenin	down
	Dvl1	dishevelled, dsh homolog 1 (Drosophila)	mouse homolog contributes to social and sensorimotor behavior	down
TNF-appha/NF-kB singnal	Smarca4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	mouse homolog is a catalytic subunit of mammalian chromatin-remodeling complexes	down
	Akap8	A kinase (PRKA) anchor protein 8	scaffolding protein that is involved in targeting type II cAMP-dependent protein kinase for cAMP-responsive nuclear events	down
Wnt_NetPath_8	Dvl1	dishevelled, dsh homolog 1 (Drosophila)	mouse homolog contributes to social and sensorimotor behavior	down used 3 times
	Axin2	axin2	inhibits axis formation; acts as a negative regulator of the Wnt signaling pathway by inducing GSK-3beta-dependent phosphorylation of beta-catenin	down

Supplemental Data Table S4. The Affymetrix ID and the Name/Description of the Entire List of Significantly Changed Genes Resulting from D-Serine Exposure

Up-Regulated Genes	
AFFY_ID	**Gene Name**
1367452_at	smt3 suppressor of mif two 3 homolog 2 (yeast)
1367454_at	coatomer protein complex, subunit beta 2 (beta prime)
1367462_at	calpain, small subunit 1
1367472_at	similar to ubiquitin-protein ligase (ec 6.3.2.19) e1 - mouse
1367473_at	translocase of outer mitochondrial membrane 22 homolog (yeast)
1367475_at, 1370825_a_at	cell division cycle 42 homolog (s. cerevisiae)
1367488_at	similar to ankyrin repeat domain protein 17 isoform b
1367495_at	similar to prefoldin 4
1367514_at	similar to riken cdna 9030624j02
1367525_at	thyroid hormone receptor associated protein 3
1367531_at	eukaryotic translation initiation factor 4h
1367560_at	acidic ribosomal phosphoprotein p0
1367562_at, 1367563_at	secreted acidic cysteine rich glycoprotein
1367567_at	ribosomal protein l6
1367568_a_at	matrix gla protein
1367569_at, 1388244_s_at, 1371189_x_at	laminin receptor 1 (ribosomal protein sa)
1367573_at	ribosomal protein s6
1367574_at	vimentin
1367578_at	peroxiredoxin 2
1367579_a_at	similar to tubulin alpha-2 chain (alpha-tubulin 2)
1367579_a_at	tubulin, alpha 6
1367579_a_at	tubulin, alpha 1
1367580_at	ribosomal protein l10a
1367581_a_at	secreted phosphoprotein 1
1367582_at	ribosomal protein l29
1367584_at	annexin a2
1367586_at	lactate dehydrogenase a
1367590_at	ran, member ras oncogene family
1367593_at	selenoprotein w, muscle 1
1367594_at	biglycan
1367596_at	ribosomal protein s26
1367597_at	ribosomal protein s8
1367604_at	cysteine-rich protein 2
1367605_at	profilin 1
1367614_at	annexin a1
1367617_at	aldolase a
1367618_a_at	discs, large homolog 5 (drosophila) (predicted)
1367623_at	ribosomal protein l18
1367628_at	lectin, galactose binding, soluble 1
1367634_at	ribosomal protein l31

Supplemental Data Table S4. Continued.

1367639_a_at	ribosomal protein s2
1367640_at	ribosomal protein s12
1367645_at	ribosomal protein s17
1367646_at	cathepsin b
1367651_at	cathepsin d
1367655_at	similar to thymosin, beta 10
1367657_at	b-cell translocation gene 1, anti-proliferative
1367663_at	protease (prosome, macropain) 28 subunit, alpha
1367666_at	heterogeneous nuclear ribonucleoprotein h1
1367671_at	proliferating cell nuclear antigen
1367676_at	high mobility group box 2
1367676_at	similar to high mobility group protein 2 (hmg-2)
1367676_at	similar to high mobility group protein 2 (hmg-2)
1367681_at	cd151 antigen
1367685_at	ribosomal protein s27a
1367690_at	signal sequence receptor 4
1367691_at	protein kinase c, delta binding protein
1367693_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
1367698_a_at	septin 9
1367701_at	receptor (calcitonin) activity modifying protein 2
1367704_at	adaptor-related protein complex 2, beta 1 subunit
1367710_at	proteasome (prosome, macropain) 28 subunit, beta
1367712_at	tissue inhibitor of metalloproteinase 1
1367715_at	tumor necrosis factor receptor superfamily, member 1a
1367722_at	dipeptidylpeptidase 7
1367732_at, 1375705_at	guanine nucleotide binding protein, beta 1
1367744_at	melanoma antigen, family d, 2
1367746_a_at	flotillin 2
1367760_at	mitogen activated protein kinase kinase 1
1367768_at	latexin
1367769_at	polymerase (rna) ii (dna directed) polypeptide g
1367772_at	chloride channel, nucleotide-sensitive, 1a
1367780_at	pituitary tumor-transforming 1
1367784_a_at	clusterin
1367786_at	proteosome (prosome, macropain) subunit, beta type 8
1367790_at	staphylococcal nuclease domain containing 1
1367794_at	alpha-2-macroglobulin
1367800_at	plasminogen activator, tissue
1367803_at	nucleoporin 54
1367805_at, 1367806_at	glutaminase
1367816_at	homeobox only domain
1367827_at	protein phosphatase 2a, catalytic subunit, beta isoform
1367844_at	guanine nucleotide binding protein, alpha inhibiting 2
1367846_at	s100 calcium-binding protein a4
1367849_at	syndecan 1
1367854_at	atp citrate lyase

Supplemental Data Table S4. Continued.

1367856_at	glucose-6-phosphate dehydrogenase
1367857_at	fatty acid desaturase 1
1367860_a_at	matrix metalloproteinase 14 (membrane-inserted)
1367881_at	protein tyrosine phosphatase, non-receptor type substrate 1
1367890_at	caspase 2
1367895_at, 1398797_at	heterogeneous nuclear ribonucleoprotein k
1367896_at	carbonic anhydrase 3
1367899_at	coagulation factor ii (thrombin) receptor
1367900_at	glycogenin 1
1367901_at	glucuronidase, beta
1367914_at	epithelial membrane protein 3
1367922_at	a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)
1367925_at	major vault protein
1367931_a_at	polypyrimidine tract binding protein 1
1367957_at	regulator of g-protein signalling 3
1367967_at	leprecan 1
1367972_at	cullin associated and neddylation disassociated 1
1367974_at	annexin a3
1367986_at	prostaglandin f2 receptor negative regulator
1368004_at	mitochondrial ribosomal protein l23
1368005_at	inositol 1, 4, 5-triphosphate receptor 3
1368013_at	dna-damage-inducible transcript 4-like
1368022_at	inositol polyphosphate phosphatase-like 1
1368035_a_at, 1368036_at	protein tyrosine phosphatase, receptor type, f
1368037_at	carbonyl reductase 1
1368049_at	t-complex protein 1
1368052_at	tetraspanin 8
1368053_at	par-3 (partitioning defective 3) homolog (c. elegans)
1368055_a_at	lamin a
1368062_at	adaptor-related protein complex 3, mu 1 subunit
1368073_at	interferon regulatory factor 1
1368082_at	solute carrier family 4, member 2
1368083_at	cyclin h
1368118_at	b-cell cll/lymphoma 10
1368143_at	annexin a7
1368168_at	solute carrier family 34 (sodium phosphate), member 2
1368173_at	nucleolar protein 5
1368187_at	glycoprotein (transmembrane) nmb
1368199_at	nucleoporin 88
1368204_at	ligase i, dna, atp-dependent
1368204_at	ligase i, dna, atp-dependent (predicted)
1368211_at	ribosomal protein s14
1368217_at	rala binding protein 1
1368223_at	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1
1368250_at	tektin 1

Supplemental Data Table S4. Continued.

1368251_at	janus kinase 3
1368260_at	aurora kinase b
1368280_at, 1374778_at	cathepsin c
1368308_at	myelocytomatosis viral oncogene homolog (avian)
1368321_at	early growth response 1
1368361_a_at	protein tyrosine phosphatase, non-receptor type 2
1368368_a_at	liver-specific bhlh-zip transcription factor 7
1368392_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
1368404_at	drebrin 1
1368464_at	macrophage galactose n-acetyl-galactosamine specific lectin 1
1368466_a_at	outer dense fiber of sperm tails 2
1368490_at	cd14 antigen
1368522_at	timeless homolog (drosophila)
1368540_at	trophoblast glycoprotein
1368571_at	cytoplasmic linker 2
1368573_at, 1372550_at	karyopherin (importin) beta 1
1368658_at	ciliary neurotrophic factor
1368669_at	uncoupling protein 2
1368687_at	testis specific protein kinase 1
1368702_at	prkc, apoptosis, wt1, regulator
1368732_at	transporter 2, atp-binding cassette, sub-family b (mdr/tap)
1368745_at	solute carrier family 10, member 2
1368751_at	potassium voltage-gated channel, delayed-rectifier, subfamily s, member 3
1368762_at	ubiquitin d
1368790_at	serine (or cysteine) proteinase inhibitor, clade a (alpha-1 antiproteinase, antitrypsin), member 10
1368799_at	baculoviral iap repeat-containing 5
1368808_at, 1368809_at	cap, adenylate cyclase-associated protein 1 (yeast)
1368824_at	caldesmon 1
1368829_at	fibrillin 1
1368834_at	calcium/calmodulin-dependent protein kinase ii, delta
1368838_at, 1371653_at	tropomyosin 4
1368840_at	lr8 protein
1368862_at, 1383126_at	thymoma viral proto-oncogene 1
1368869_at	a kinase (prka) anchor protein (gravin) 12
1368871_at, 1375673_at	mitogen activated protein kinase kinase kinase 1
1368888_a_at, 1388027_a_at	reticulon 4
1368908_at	annexin a4
1368914_at	runt related transcription factor 1
1368921_a_at, 1387952_a_at, 1390659_at	cd44 antigen

Supplemental Data Table S4. Continued.

1368990_at	cytochrome p450, family 1, subfamily b, polypeptide 1
1369013_a_at	mitochondrial ribosomal protein l17
1369029_at	phospholipid scramblase 1
1369077_at	n-acylsphingosine amidohydrolase 1
1369209_at	p34 protein
1369262_at	caspase 8
1369294_at	bone marrow stromal cell antigen 1
1369312_a_at, 1374646_at	casein kinase 1, alpha 1
1369644_at	latrophilin 2
1369712_at	serine/threonine kinase 3 (ste20 homolog, yeast)
1369720_at	myosin ib
1369931_at	similar to pyruvate kinase (ec 2.7.1.40) isozyme m2 - rat
1369934_at	peptidylprolyl isomerase b
1369936_at, 1370246_at, 1372770_at	calmodulin 1
1369941_at	death-associated protein
1369943_at	transglutaminase 2, c polypeptide
1369944_at	marcks-like protein
1369950_at	cyclin-dependent kinase 4
1369952_at	poly(a) binding protein, cytoplasmic 1
1369953_a_at	cd24 antigen
1369955_at, 1376099_at	collagen, type v, alpha 1
1369958_at	rhob gene
1369964_at	coronin, actin binding protein 1a
1369966_a_at	ribosomal protein s24
1369968_at	pleiotrophin
1369969_at	adp-ribosyltransferase 1
1369971_a_at	heterogeneous nuclear ribonucleoprotein d
1369976_at	dynein, cytoplasmic, light chain 1
1369978_at	phosphoribosyl pyrophosphate synthetase-associated protein 2
1369979_at	src family associated phosphoprotein 2
1369980_s_at	myosin phosphatase-rho interacting protein
1369991_at	signal peptidase complex 18kd
1369996_at	polymerase (rna) ii (dna directed) polypeptide f
1370000_at	nucleobindin 2
1370003_at	eukaryotic translation elongation factor 2
1370004_at	h2a histone family, member y
1370007_at	protein disulfide isomerase associated 4
1370014_at	syntaxin 4a (placental)
1370054_at	cyclin-dependent kinase inhibitor 2c (p18, inhibits cdk4)
1370057_at	cysteine and glycine-rich protein 1
1370112_at	phosphatase and tensin homolog
1370130_at, 1399027_at	ras homolog gene family, member a
1370141_at	myeloid cell leukemia sequence 1

Supplemental Data Table S4. Continued.

1370155_at, 1387854_at	procollagen, type i, alpha 2
1370156_at	prion protein
1370168_at, 1387862_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide
1370170_at	heterogeneous nuclear ribonucleoprotein u
1370186_at	proteosome (prosome, macropain) subunit, beta type 9
1370188_at, 1370189_at	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, drosophila)
1370190_at, 1398888_at, 1398849_at	h3 histone, family 3b
1370199_at	nucleobindin 1
1370213_at	nuclease sensitive element binding protein 1
1370224_at, 1371781_at	signal transducer and activator of transcription 3
1370234_at	fibronectin 1
1370243_a_at	prothymosin alpha
1370249_at	benzodiazepine receptor, peripheral
1370250_at	similar to riken cdna a930001m12 gene
1370250_at, 1388474_at	ubiquitin-conjugating enzyme e2i
1370252_at	arginine vasopressin-induced 1
1370253_at	ribosomal protein l22
1370258_at	basic leucine zipper and w2 domains 2
1370280_at	hypoxanthine guanine phosphoribosyl transferase
1370287_a_at	tropomyosin 1, alpha
1370290_at, 1387892_at	tubulin, beta 5
1370294_a_at	cell division cycle 20 homolog (s. cerevisiae)
1370297_at	polo-like kinase 1 (drosophila)
1370301_at	matrix metallopeptidase 2
1370307_at	agrin
1370308_at	rs21-c6 protein
1370309_a_at	heterogeneous nuclear ribonucleoprotein a/b
1370339_at, 1398303_s_at, 1387918_at, 1370340_x_at, 1371239_s_at	tropomyosin 3, gamma
1370346_at	cyclin b1
1370347_at	pdz and lim domain 7
1370348_at	ninjurin 1
1370376_a_at	cold shock domain protein a
1370399_at	cytochrome p450, family 4, subfamily b, polypeptide 1
1370408_at	putative small membrane protein nid67
1370461_at, 1370462_at	hyaluronan mediated motility receptor

Supplemental Data Table S4. Continued.

1370527_a_at, 1373332_at	casein kinase 1, delta
1370561_at	igb3 synthase
1370571_at, 1373734_at	solute carrier organic anion transporter family, member 3a1
1370585_a_at	protein kinase c, beta 1
1370599_a_at, 1387901_at	protein tyrosine phosphatase, receptor type, d
1370678_s_at	monoamine oxidase a
1370752_a_at	tumor protein p53
1370807_at	vacuole membrane protein 1
1370813_at	glutathione s-transferase, mu 5
1370826_at	nucleosome assembly protein 1-like 1
1370864_at, 1388116_at	collagen, type 1, alpha 1
1370867_at, 1398863_at	guanine nucleotide binding protein, beta polypeptide 2
1370871_at	hypothetical gene supported by y16641; y16641
1370876_at	neurofascin
1370880_at	ribonuclease/angiogenin inhibitor 1
1370885_at	cathepsin z
1370887_at	transforming growth factor beta 1 induced transcript 1
1370890_at	arp3 actin-related protein 3 homolog (yeast)
1370891_at	cd48 antigen
1370894_at	claudin 7
1370895_at, 1373463_at	collagen, type v, alpha 2
1370898_at	stannin
1370899_at, 1388132_at	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)
1370909_at	nucleoporin 62
1370920_at	serine/arginine-rich protein specific kinase 2 (predicted)
1370927_at	procollagen, type xii, alpha 1
1370928_at	lps-induced tn factor
1370933_at	myosin ie
1370935_at, 1373054_at	cdw92 antigen
1370940_at	tight junction protein 2
1370947_at	hypothetical protein rda279
1370959_at	collagen, type iii, alpha 1
1370968_at	nuclear factor of kappa light chain gene enhancer in b-cells 1, p105
1370976_at	ras-gtpase-activating protein sh3-domain binding protein
1370999_at	sperm associated antigen 5
1371021_at, 1375412_at	arylsulfatase b
1371024_at	cut-like 1 (drosophila)
1371040_at	solute carrier family 1, member 7
1371073_at	udp-gal:betaglcnac beta 1,4- galactosyltransferase, polypeptide 1 (mapped)
1371074_a_at	mini chromosome maintenance deficient 6 (s. cerevisiae)

Supplemental Data Table S4. Continued.

1371101_at	receptor-like tyrosine kinase
1371125_at	kinesin heavy chain family, member 2
1371189_x_at	similar to 40s ribosomal protein sa (p40) (34/67 kda laminin receptor)
1371189_x_at	similar to ribosomal protein sa
1371244_at	adenine phosphoribosyl transferase (predicted)
1371246_at	nuclear transport factor 2
1371295_at	ribosomal protein s20
1371299_at	ribosomal protein s3
1371300_at	ribosomal protein l3
1371305_at	ribosomal protein l8
1371308_at	ribosomal protein s4, x-linked
1371310_s_at	serine (or cysteine) proteinase inhibitor, clade h, member 1
1371314_at	neural precursor cell expressed, developmentally down-regulated gene 4a
1371322_at	laminin, gamma 1
1371327_a_at	similar to actin, cytoplasmic 2 (gamma-actin)
1371327_a_at	actin, gamma, cytoplasmic
1371330_at	ribosomal protein l11
1371340_at	similar to 60s acidic ribosomal protein p2
1371340_at	ribosomal protein, large p2
1371341_at	small nuclear ribonucleoprotein d2 (predicted)
1371344_at	ribosomal protein l27a (predicted)
1371349_at	similar to collagen alpha1 type vi-precursor
1371351_at	similar to rna polymerase 1-3
1371352_at	high mobility group nucleosomal binding domain 2
1371365_at	similar to ubiquitin-conjugating enzyme e2s
1371369_at	procollagen, type vi, alpha 2
1371377_at	ribosomal protein s19
1371382_at	similar to filamin a (alpha-filamin) (filamin 1) (endothelial actin-binding protein) (actin-binding protein 280) (abp-280) (nonmuscle filamin)
1371386_at	similar to protein c9orf10 (predicted)
1371390_at	tubulin, beta, 2
1371391_at	thioredoxin domain containing 5 (predicted)
1371395_at	chromobox homolog 3 (hp1 gamma homolog, drosophila)
1371411_at	plexin b2
1371414_at	gelsolin
1371422_at	morf-related gene x
1371429_at	dystroglycan 1
1371432_at	vesicle amine transport protein 1 homolog (t californica)
1371435_at	nascent-polypeptide-associated complex alpha polypeptide (predicted)
1371441_at	phosphoprotein enriched in astrocytes 15
1371445_at	similar to ribosome-binding protein p34 - rat
1371465_at	cortactin isoform b
1371474_at	mitochondrial carrier homolog 1 (c. elegans)
1371475_at	ribonuclease, rnase a family 4
1371485_at	sh3 multiple domains 1 (predicted)
1371486_at	u1 small nuclear ribonucleoprotein 1c (predicted)
1371487_at	sh3 domain binding glutamic acid-rich protein-like 3 (predicted)
1371495_at	cation-dependent mannose-6-phosphate receptor

Supplemental Data Table S4. Continued.

1371499_at	cd9 antigen
1371500_at	latent transforming growth factor beta binding protein 4
1371509_at	transforming growth factor beta regulated gene 1
1371511_at	actin related protein 2/3 complex, subunit 2 (predicted)
1371530_at	keratin complex 2, basic, gene 8
1371537_at	udp-gal:betaglcnac beta 1,4-galactosyltransferase, polypeptide 5 (predicted)
1371544_at	similar to enhancer of rudimentary homolog
1371558_at	nischarin
1371563_at	similar to cg9135-pa (predicted)
1371573_at	large subunit ribosomal protein l36a
1371596_at	ribonucleic acid binding protein s1
1371602_at	similar to tetraspan net-5 (predicted)
1371610_at	tankyrase, trf1-interacting ankyrin-related adp-ribose polymerase (predicted)
1371611_at	exostoses (multiple) 2 (predicted)
1371612_at	trna splicing endonuclease 34 homolog
1371613_at	engulfment and cell motility 2, ced-12 homolog (c. elegans)
1371622_at	similar to candidate tumor suppressor ovca2
1371627_at	angiomotin-like 1 (predicted)
1371632_at	selectin, platelet (p-selectin) ligand (predicted)
1371641_at	chaperonin subunit 7 (eta) (predicted)
1371646_at	phosphogluconate dehydrogenase (mapped)
1371652_at	,gb:bf550566 /db_xref=gi:11660296 /db_xref=ui-r-c0-jl-a-08-0-ui.r1 /clone=ui-r-c0-jl-a-08-0-ui /fea=est /cnt=21 /tid=rn.14503.1 /tier=stack /stk=18 /ug=rn.14503 /ug_title=ests
1371657_at	ubiquitin-like 1 (sentrin) activating enzyme e1b
1371659_at	ras homolog gene family, member c (predicted)
1371662_at	lysyl-trna synthetase
1371676_at	longevity assurance homolog 5 (s. cerevisiae) (predicted)
1371683_at	lsm4 homolog, u6 small nuclear rna associated (s. cerevisiae) (predicted)
1371688_at	translocation associated membrane protein 1
1371713_at	v-abl abelson murine leukemia viral oncogene homolog 1 (mapped)
1371719_at	bromodomain-containing 2
1371724_at	small fragment nuclease
1371761_at	ribosomal protein l34 (predicted)
1371774_at	spermidine/spermine n1-acetyl transferase (mapped)
1371776_at	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1
1371777_at	poly a binding protein, cytoplasmic 4
1371780_at	kdel (lys-asp-glu-leu) endoplasmic reticulum protein retention receptor 2
1371782_at	nipsnap-related protein
1371785_at	tumor necrosis factor receptor superfamily, member 12a
1371786_at	tripartite motif-containing 35
1371790_at	mitochondrial ribosomal protein l45 (predicted)
1371803_at	gm2 ganglioside activator protein
1371821_at	was protein family, member 2
1371826_at	,gb:bm390536 /db_xref=gi:18190589 /db_xref=ui-r-cn1-cjr-c-13-0-ui.s1 /clone=ui-r-cn1-cjr-c-13-0-ui /fea=est /cnt=16 /tid=rn.15171.1 /tier=stack /stk=16 /ug=rn.15171 /ug_title=ests
1371826_at	btb (poz) domain containing 14b
1371830_at	ubiquitin-like 1 (sentrin) activating enzyme e1a

Supplemental Data Table S4. Continued.

1371838_at	similar to splicing factor, arginine/serine-rich 2
1371841_at	myotrophin
1371847_at	similar to cartilage-associated protein precursor
1371847_at	cartilage associated protein (predicted)
1371857_at	potassium channel tetramerization domain containing 10
1371861_at	,gb:be117558 /db_xref=gi:8509663 /db_xref=ui-r-bs1-ayk-c-05-0-ui.s1 /clone=ui-r-bs1-ayk-c-05-0-ui /fea=est /cnt=20 /tid=rn.19802.1 /tier=stack /stk=15 /ug=rn.19802 /ug_title=ests, moderately similar to t13963 formin related protein, lymphocyte specific - mouse (m.musculus)
1371871_at	rab12, member ras oncogene family
1371878_at	mastermind like 1 (drosophila) (predicted)
1371883_at	monocyte to macrophage differentiation-associated
1371887_at	similar to high mobility group protein homolog hmg4
1371914_at	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1
1371928_at	cell division cycle associated 8
1371936_at	eukaryotic translation initiation factor 4a1
1371938_at	gpi-anchored membrane protein 1
1371958_at	poly(a) binding protein, nuclear 1
1371970_at	similar to expressed sequence aw413625
1371973_at	eukaryotic translation initiation factor 3, subunit 6
1371977_at	actin related protein 2/3 complex, subunit 3 (predicted)
1371983_at	similar to riken cdna 1300006c06
1371987_at	polymerase (dna directed) sigma (predicted)
1372002_at	gap junction membrane channel protein alpha 1
1372003_at	similar to cg17660-pa (predicted)
1372004_at	heme binding protein 1 (predicted)
1372006_at	,gb:bm391274 /db_xref=gi:18191327 /db_xref=ui-r-dy0-ckq-b-09-0-ui.s1 /clone=ui-r-dy0-ckq-b-09-0-ui /fea=est /cnt=16 /tid=rn.954.1 /tier=stack /stk=14 /ug=rn.954 /ug_title=ests
1372029_at	similar to mannose-6-phosphate receptor binding protein 1
1372032_at	neuroblastoma ras oncogene
1372050_at	similar to hypothetical protein mgc38524 (predicted)
1372052_at	budding uninhibited by benzimidazoles 3 homolog (s. cerevisiae)
1372056_at	chemokine-like factor super family 6
1372064_at	similar to chemokine (c-x-c motif) ligand 16
1372067_at	thioredoxin domain containing 1
1372075_at	similar to dj862k6.2.2 (splicing factor, arginine/serine-rich 6 (srp55-2)(isoform 2))
1372081_at	,gb:bi299305 /db_xref=gi:14975585 /db_xref=ui-r-cv2-cht-f-02-0-ui.s1 /clone=ui-r-cv2-cht-f-02-0-ui /fea=est /cnt=21 /tid=rn.18074.1 /tier=stack /stk=13 /ug=rn.18074 /ug_title=ests
1372082_at	unknown (protein for mgc:72598)
1372091_at	mid1 interacting g12-like protein
1372096_at	oxidative-stress responsive 1 (predicted)
1372112_at	similar to 9230105e10rik protein
1372125_at	glutathione peroxidase 7 (predicted)
1372126_at	,gb:bi288075 /db_xref=gi:14944301 /db_xref=ui-r-cs0s-cbk-a-10-0-ui.s2 /clone=ui-r-cs0s-cbk-a-10-0-ui /fea=est /cnt=19 /tid=rn.17074.1 /tier=stack /stk=13 /ug=rn.17074 /ug_title=ests

Supplemental Data Table S4. Continued.

1372127_at	ubiquitin-associated protein 2 (predicted)
1372133_at	related ras viral (r-ras) oncogene homolog 2
1372135_at	protein tyrosine kinase 9-like (a6-related protein) (predicted)
1372148_at	comm domain containing 2 (predicted)
1372151_at	transcription elongation regulator 1 (ca150) (predicted)
1372155_at	tripartite motif protein 28
1372168_s_at	insulin-like growth factor binding protein 6
1372181_at	replication protein a1
1372182_at	phosphofructokinase, platelet
1372183_at	karyopherin (importin) alpha 1
1372187_at	protein kinase c, nu
1372234_at	similar to lix1 homolog (mouse) like
1372241_at	ornithine decarboxylase antizyme 1
1372246_at	osteoclast stimulating factor 1
1372249_at	ac1254
1372250_at	scf apoptosis response protein 1
1372251_at	rna binding motif protein 5
1372273_at	glycophorin c (gerbich blood group)
1372286_at	similar to transmembrane 4 superfamily member 6
1372294_at	pe responsive protein c64
1372303_at	similar to 0910001a06rik protein (predicted)
1372327_at	myelin basic protein expression factor 2, repressor
1372332_at	,gb:ai170687 /db_xref=gi:3710727 /db_xref=est216623 /clone=rmuaz96 /fea=est /cnt=14 /tid=rn.13655.1 /tier=stack /stk=12 /ug=rn.13655 /ug_title=ests
1372333_at	similar to small nuclear ribonucleoprotein e
1372333_at	small nuclear ribonucleoprotein e (predicted)
1372343_at	exosome component 8 (predicted)
1372352_at	arginine-rich, mutated in early stage tumors (predicted)
1372364_a_at	similar to n-terminal asparagine amidohydrolase
1372377_at	dead (asp-glu-ala-asp) box polypeptide 41 (predicted)
1372380_at, 1375898_at	similar to rna binding protein gene with multiple splicing
1372391_at	similar to riken cdna 1500016h10 (predicted)
1372401_at, 1372402_at	n-acetylneuraminic acid synthase (sialic acid synthase) (predicted)
1372406_at	similar to dna replication licensing factor mcm3 (dna polymerase alpha holoenzyme-associated protein p1) (p1-mcm3)
1372406_at	minichromosome maintenance deficient 3 (s. cerevisiae) (predicted)
1372439_at, 1373245_at	procollagen, type iv, alpha 1
1372441_at	chromodomain helicase dna binding protein 4
1372459_at	vasodilator-stimulated phosphoprotein (predicted)
1372460_at, 1372461_at	loc499767
1372461_at	set translocation (predicted)
1372466_at	transforming growth factor, beta receptor ii
1372473_at	tight junction protein 1 (predicted)
1372476_at	fatty acid desaturase 3

Supplemental Data Table S4. Continued.

1372500_at	tropomodulin 3
1372501_at	splicing factor 3b, subunit 3 (predicted)
1372511_at	daz associated protein 2
1372513_at	ras-related c3 botulinum toxin substrate 1 (rho family, small gtp binding protein rac1)
1372516_at	kinesin family member 22
1372517_at	peptidylprolyl isomerase (cyclophilin)-like 1
1372519_at	nucleoporin 93
1372530_at	similar to hcf
1372542_at	quaking homolog, kh domain rna binding (mouse)
1372543_at	similar to riken cdna 2610029g23
1372546_at	mitogen-activated protein kinase-activated protein kinase 3
1372552_at	dmt1-associated protein
1372564_at	v-ets erythroblastosis virus e26 oncogene homolog 2 (avian) (mapped)
1372569_at	four and a half lim domains 3 (predicted)
1372577_at	actin related protein 2/3 complex, subunit 4 (predicted)
1372599_at	microsomal glutathione s-transferase 2 (predicted)
1372606_at	cell division cycle associated 7
1372609_at	protein phosphatase 2, regulatory subunit b (b56), delta isoform
1372631_at, 1389858_at	thymidine kinase 1
1372634_at	adp-ribosylhydrolase like 2 (predicted)
1372643_at	similar to protein 4.1g
1372667_at	similar to riken cdna 1110059e24
1372668_at	lim domains containing 1 (predicted)
1372685_at	cyclin-dependent kinase inhibitor 3 (predicted)
1372686_at	hypothetical loc291080 (predicted)
1372691_at	uridine phosphorylase 1
1372704_at	similar to riken cdna 2310008m10
1372706_at	hexosaminidase b
1372709_at	b-cell receptor-associated protein bap29
1372722_at	dnaj (hsp40) homolog, subfamily b, member 4
1372723_at, 1373972_at	importin 9 (predicted)
1372739_at	sarcoma amplified sequence
1372749_at	rna-binding protein 12
1372773_at	neural proliferation, differentiation and control, 1
1372778_at	solute carrier family 39 (zinc transporter), member 1 (predicted)
1372784_at	similar to muf1-pending protein
1372801_at	comm domain containing 10
1372805_at	loc363015 (predicted)
1372810_at	heterogeneous nuclear ribonucleoprotein d-like
1372811_at	similar to kinectin
1372815_at	mago-nashi homolog, proliferation-associated (drosophila) (predicted)
1372817_at	zinc finger protein 260
1372837_at	wd repeat and fyve domain containing 2 (predicted)
1372870_at	kdel (lys-asp-glu-leu) endoplasmic reticulum protein retention receptor 3 (predicted)
1372877_at	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3

Supplemental Data Table S4. Continued.

1372886_at	transforming acidic coiled coil 3
1372890_at	sphingosine phosphate lyase 1
1372897_at	hypothetical gene supported by nm_175869
1372904_at	mob1, mps one binder kinase activator-like 2b (yeast) (predicted)
1372906_at	similar to hypothetical protein mgc40841; similar to hypothetical protein mgc4707
1372914_at	lymphotoxin b receptor
1372919_at	similar to putative lysophosphatidic acid acyltransferase
1372930_at	sp110 nuclear body protein
1372931_at	similar to dximx39e protein
1372934_at	similar to 1700019e19rik protein (predicted)
1372938_at	similar to riken cdna 6330509g02
1372949_at	septin 6 (predicted)
1372964_at	at rich interactive domain 5b (mrf1 like) (predicted)
1372968_at	set binding factor 1 (predicted)
1372990_at	camp responsive element binding protein 3
1373024_at	adaptor-related protein complex 3, sigma 1 subunit (predicted)
1373026_at	similar to riken cdna 2410030k01 (predicted)
1373030_at	loc501594
1373034_at	tryptophan rich basic protein
1373035_at	similar to cdna sequence bc017158
1373037_at	ubiquitin-conjugating enzyme e2l 6
1373040_at	eukaryotic translation initiation factor 3, subunit 5 (epsilon) (predicted)
1373044_at	similar to dendritic cell protein ga17
1373047_at	protein kinase c, lambda
1373052_at	phosducin-like 3
1373072_at	,gb:ai170552 /db_xref=gi:3710592 /db_xref=est216483 /clone=rlucq61 /fea=est /cnt=14 /tid=rn.1897.1 /tier=stack /stk=9 /ug=rn.1897 /ug_title=ests
1373087_at	axotrophin
1373103_at	metastasis-associated gene family, member 2
1373114_at	,gb:ai408442 /db_xref=gi:4251946 /db_xref=est236732 /clone=roveo36 /fea=est /cnt=12 /tid=rn.18597.1 /tier=stack /stk=9 /ug=rn.18597 /ug_title=ests
1373128_at	reticulocalbin 3, ef-hand calcium binding domain
1373140_at	interleukin 6 signal transducer
1373143_at	similar to hypothetical protein flj10652
1373150_at	catechol-o-methyltransferase domain containing 1 (predicted)
1373151_at	similar to lipoma hmgic fusion partner
1373153_at	myelin oligodendrocyte glycoprotein
1373156_at	similar to armadillo repeat protein alex2
1373164_at, 1387502_at	serine/threonine kinase 17b (apoptosis-inducing)
1373195_at	fusion (involved in t(12;16) in malignant liposarcoma)
1373204_at	hypothetical loc297077
1373206_at, 1373416_at	similar to fad104 (predicted)
1373210_at	laminin b1 subunit 1 (predicted)
1373234_at	,gb:bi277492 /db_xref=gi:14923420 /db_xref=ui-r-cy0-bxq-g-07-0-ui.s1 /clone=ui-r-cy0-bxq-g-07-0-ui /fea=est /cnt=10 /tid=rn.34796.1 /tier=stack /stk=9 /ug=rn.34796 /ug_title=ests

Supplemental Data Table S4. Continued.

1373262_at	similar to 2310014h01rik protein (predicted)
1373268_at	microtubule-associated protein 4
1373269_at	,gb:ai407751 /db_xref=gi:4251255 /db_xref=est236041 /clone=rovea21 /fea=est /cnt=10 /tid=rn.2560.1 /tier=stack /stk=9 /ug=rn.2560 /ug_title=ests
1373286_at	csx-associated lim
1373288_at	suppression of tumorigenicity 5 (predicted)
1373290_at	similar to ezh2 protein
1373363_at	microtubule-associated protein 1b
1373364_at	eukaryotic translation initiation factor 4 gamma, 3 (predicted)
1373375_at	rab6 interacting protein 1 (predicted)
1373385_at	similar to mahogunin, ring finger 1; mahoganoid
1373392_at	tpa regulated locus
1373393_at	similar to ext1
1373399_at	wd repeat domain 6
1373401_at	tenascin c
1373403_at	,gb:ai230625 /db_xref=gi:3814512 /db_xref=est227320 /clone=remcz18 /fea=est /cnt=14 /tid=rn.24073.1 /tier=stack /stk=8 /ug=rn.24073 /ug_title=ests
1373454_at	similar to riken cdna 0610037p05
1373460_at	d-serine modulator-1
1373499_at	growth arrest specific 5
1373504_at	gli pathogenesis-related 1 (glioma)
1373512_at	ilvb (bacterial acetolactate synthase)-like (predicted)
1373514_at	similar to chromosome 17 open reading frame 27 (predicted)
1373535_at	enabled homolog (drosophila)
1373540_at	heterogeneous nuclear ribonucleoprotein a2/b1 (predicted)
1373541_at	rho guanine nucleotide exchange factor (gef) 17 (predicted)
1373555_at	dynactin 4
1373556_at	similar to cg14903-pa
1373557_at	minichromosome maintenance deficient 4 homolog (s. cerevisiae)
1373557_at	similar to mcdc21 protein
1373565_at	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
1373592_at	similar to spi6
1373595_at	similar to riken cdna 1200015a22
1373616_at	loc499369
1373629_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 (predicted)
1373657_at	solute carrier family 31, member 2
1373658_at	rac gtpase-activating protein 1 (predicted)
1373673_at	,gb:bf284593 /db_xref=gi:11215663 /db_xref=est449184 /clone=rgies62 /fea=est /cnt=9 /tid=rn.28805.1 /tier=stack /stk=8 /ug=rn.28805 /ug_title=ests
1373703_at	,gb:be113247 /db_xref=gi:8505352 /db_xref=ui-r-bj1-awd-c-03-0-ui.s1 /clone=ui-r-bj1-awd-c-03-0-ui /fea=est /cnt=8 /tid=rn.13320.1 /tier=stack /stk=8 /ug=rn.13320 /ug_title=ests
1373732_at	acid phosphatase 6, lysophosphatidic
1373750_at	leprecan-like 2 (predicted)
1373772_at	dna (cytosine-5-)-methyltransferase 1
1373822_at	similar to riken cdna 1110025l05
1373823_at	similar to cyclin-dependent kinases regulatory subunit 2 (cks-2)

Supplemental Data Table S4. Continued.

1373829_at	fibroblast growth factor receptor 2
1373853_at	similar to hypothetical protein mgc15716
1373860_at	sry-box containing gene 4 (predicted)
1373867_at	,gb:bi289360 /db_xref=gi:14946842 /db_xref=ui-r-dk0-cfg-a-07-0-ui.s1 /clone=ui-r-dk0-cfg-a-07-0-ui /fea=est /cnt=15 /tid=rn.17403.1 /tier=stack /stk=7 /ug=rn.17403 /ug_title=ests
1373868_at	bcl2-associated transcription factor 1
1373870_at	similar to riken cdna 2810405j04
1373897_at	lamin b1
1373905_at	heterogeneous nuclear ribonucleoprotein r
1373951_at, 1386905_at	protein kinase, camp dependent regulatory, type i, alpha
1373958_at	similar to alex3 protein
1373966_at	retinoic acid induced 1 (predicted)
1373984_at	solute carrier family 39 (zinc transporter), member 14 (predicted)
1374015_at	,gb:bf281697 /db_xref=gi:11212767 /db_xref=est446288 /clone=rgiap26 /fea=est /cnt=9 /tid=rn.7770.1 /tier=stack /stk=7 /ug=rn.7770 /ug_title=ests
1374033_at	proteasome (prosome, macropain) subunit, beta type 10
1374063_at	splicing factor, arginine/serine-rich 3 (srp20) (predicted)
1374065_at	,gb:bg378920 /db_xref=gi:13303392 /db_xref=ui-r-cv1-bvu-e-07-0-ui.s1 /clone=ui-r-cv1-bvu-e-07-0-ui /fea=est /cnt=13 /tid=rn.38245.1 /tier=stack /stk=7 /ug=rn.38245 /ug_title=ests
1374070_at	glutathione peroxidase 2
1374134_at	pctaire-motif protein kinase 2
1374181_at	similar to heterogeneous nuclear ribonucleoprotein g - human
1374198_at	b7 homlog 3
1374225_at	hypothetical protein
1374228_at	tripartite motif protein 47 (predicted)
1374265_at	similar to arylacetamide deacetylase (esterase) (predicted)
1374286_at	,gb:aa996836 /db_xref=gi:4280600 /db_xref=ui-r-c0-hg-e-02-0-ui.s1 /clone=ui-r-c0-hg-e-02-0-ui /fea=est /cnt=7 /tid=rn.8901.1 /tier=stack /stk=7 /ug=rn.8901 /ug_title=ests
1374292_at	similar to riken cdna 1110031i02
1374321_at	reticulon 3
1374368_at	,gb:bi291066 /db_xref=gi:14950263 /db_xref=ui-r-dk0-cgf-a-11-0-ui.s1 /clone=ui-r-dk0-cgf-a-11-0-ui /fea=est /cnt=7 /tid=rn.25222.1 /tier=stack /stk=7 /ug=rn.25222 /ug_title=ests
1374387_at	adp-ribosylation factor-like 6 interacting protein 5
1374388_at	ef hand domain containing 2
1374395_at, 1388150_at	exportin 1, crm1 homolog (yeast)
1374405_at, 1388119_at	heterogeneous nuclear ribonucleoprotein a3
1374442_at	splicing factor, arginine/serine rich 9
1374449_at	similar to cell division cycle associated 3
1374449_at	cell division cycle associated 3
1374453_at	,gb:aw917568 /db_xref=gi:8083322 /db_xref=est348872 /clone=rgief42 /fea=est /cnt=11 /tid=rn.12980.1 /tier=stack /stk=6 /ug=rn.12980 /ug_title=ests
1374455_at	similar to ayp1 (predicted)

Supplemental Data Table S4. Continued.

1374456_at	,gb:ai179562 /db_xref=gi:3730200 /db_xref=est223283 /clone=rspci95 /fea=est /cnt=11 /tid=rn.4141.1 /tier=stack /stk=6 /ug=rn.4141 /ug_title=ests
1374457_at	similar to serine c-palmitoyltransferase
1374499_at	tata box binding protein (tbp)-associated factor, rna polymerase i, a
1374500_at	similar to sarcoma antigen ny-sar-27
1374513_at, 1387436_at	septin 7
1374526_at	ankyrin repeat and fyve domain containing 1 (predicted)
1374537_at	carbohydrate (chondroitin) synthase 1 (predicted)
1374538_at	o-linked mannose beta1,2-n-acetylglucosaminyltransferase
1374555_at	acyl-coenzyme a binding domain containing 6
1374557_at	cg6210-like
1374571_at	similar to hypothetical protein flj20522
1374595_at	tankyrase, trf1-interacting ankyrin-related adp-ribose polymerase 2 (predicted)
1374601_at	interferon gamma receptor 2 (predicted)
1374704_at	kdel (lys-asp-glu-leu) containing 2
1374705_at	similar to type iv collagen alpha 5 chain
1374708_at	similar to rho guanine nucleotide exchange factor (gef) 10
1374718_at	similar to deltex 3-like
1374747_at	pftaire protein kinase 1 (predicted)
1374775_at	similar to mki67 protein
1374775_at	antigen identified by monoclonal antibody ki-67 (predicted)
1374775_at	similar to ki-67
1374788_at	transformation related protein 53 binding protein 1 (predicted)
1374794_at	kinesin-like 7
1374799_at	similar to mkiaa0159 protein
1374812_at	protein tyrosine phosphatase, non-receptor type 13
1374834_at	splicing factor 3b, subunit 4
1374876_at	leptin receptor overlapping transcript-like 1
1374905_at	unc-84 homolog b (c. elegans) (predicted)
1374912_at	kinesin-related protein 2
1374976_a_at	sterol o-acyltransferase 1
1375006_at	similar to riken cdna b130055l09 (predicted)
1375010_at	cd68 antigen
1375014_at	hypothetical loc301598
1375020_at	ras and rab interactor 3 (predicted)
1375060_at	similar to cc2-27 (predicted)
1375170_at	s100 calcium binding protein a11 (calizzarin) (predicted)
1375174_at, 1389483_at	similar to kiaa0877 protein (predicted)
1375181_at	similar to 60s ribosomal protein l12
1375182_at	similar to riken cdna d030028o16
1375184_at	,gb:bi281837 /db_xref=gi:14931987 /db_xref=ui-r-cu0s-cbt-b-06-0-ui.s1 /clone=ui-r-cu0s-cbt-b-06-0-ui /fea=est /cnt=27 /tid=rn.35278.1 /tier=stack /stk=16 /ug=rn.35278 /ug_title=ests
1375194_at	,gb:ai231460 /db_xref=gi:3815340 /db_xref=est228148 /clone=remdk43 /fea=est /cnt=16 /tid=rn.12107.1 /tier=stack /stk=16 /ug=rn.12107 /ug_title=ests

Supplemental Data Table S4. Continued.

1375212_at	similar to riken cdna g431002c21 (predicted)
1375216_at	poliovirus receptor-related 2 (herpesvirus entry mediator b)
1375221_at	similar to cg5554-pa
1375224_at	pleckstrin homology-like domain, family a, member 3
1375249_at	eukaryotic translation initiation factor 2c, 1 (predicted)
1375279_at	serta domain containing 2
1375299_at	dullard homolog (xenopus laevis)
1375336_at	heat shock 90kda protein 1, beta
1375338_at	rab10, member ras oncogene family
1375358_at	,gb:aa998150 /db_xref=gi:4287865 /db_xref=ui-r-c0-id-c-11-0-ui.s1 /clone=ui-r-c0-id-c-11-0-ui /fea=est /cnt=12 /tid=rn.7701.1 /tier=stack /stk=9 /ug=rn.7701 /ug_title=ests
1375414_at	taf9 rna polymerase ii, tata box binding protein (tbp)-associated factor pseudogene
1375420_at	tumor protein p53 inducible protein 11 (predicted)
1375432_at	,gb:ai171599 /db_xref=gi:4134636 /db_xref=est217566 /clone=rmubn05 /fea=est /cnt=13 /tid=rn.22355.1 /tier=stack /stk=8 /ug=rn.22355 /ug_title=ests, highly similar to csl4_human 3-5 exoribonuclease csl4 homolog (cgi-108 protein) (h.sapiens)
1375435_at	hypothetical loc308765 (predicted)
1375521_at	transcription elongation factor a (sii)-like 8
1375525_at	microtubule-associated protein, rp/eb family, member 1
1375538_at	vinculin (predicted)
1375546_at	fizzy/cell division cycle 20 related 1 (drosophila) (predicted)
1375559_at	,gb:bi283479 /db_xref=gi:14935262 /db_xref=ui-r-de0-cab-g-09-0-ui.s1 /clone=ui-r-de0-cab-g-09-0-ui /fea=est /cnt=9 /tid=rn.40945.1 /tier=stack /stk=7 /ug=rn.40945 /ug_title=ests, weakly similar to lhx5 mouse limhomeobox protein lhx5 (r.norvegicus)
1375563_at	similar to dendritic cell-derived ubiquitin-like protein (predicted)
1375612_at, 1387872_at	heterogeneous nuclear ribonucleoprotein a1
1375633_at	chloride intracellular channel 1
1375653_at	neurexin 3
1375654_at	cytoskeleton-associated protein 4 (predicted)
1375655_at	,gb:be107208 /db_xref=gi:8499313 /db_xref=ui-r-bs1-ayr-b-04-0-ui.s1 /clone=ui-r-bs1-ayr-b-04-0-ui /fea=est /cnt=12 /tid=rn.22668.1 /tier=stack /stk=6 /ug=rn.22668 /ug_title=ests, weakly similar to mlh3_human dna mismatch repair protein mlh3 (mutl protein homolog 3) (h.sapiens)
1375658_at	,gb:ai412317 /db_xref=gi:4255821 /db_xref=est240615 /clone=rbrdv25 /fea=est /cnt=11 /tid=rn.22768.1 /tier=stack /stk=6 /ug=rn.22768 /ug_title=ests
1375686_at	peptidylprolyl isomerase (cyclophilin)-like 3
1375723_at	,gb:ai385171 /db_xref=gi:4197953 /db_xref=ui-r-e0-ci-f-01-0-ui.s1 /clone=ui-r-e0-ci-f-01-0-ui /fea=est /cnt=8 /tid=rn.34293.1 /tier=stack /stk=6 /ug=rn.34293 /ug_title=ests
1375793_at	,gb:bi295700 /db_xref=gi:14959410 /db_xref=ui-r-dk0-ceu-e-12-0-ui.s1 /clone=ui-r-dk0-ceu-e-12-0-ui /fea=est /cnt=6 /tid=rn.53937.1 /tier=stack /stk=6 /ug=rn.53937 /ug_title=ests
1375845_at	similar to aig1 protein
1375848_at	paraoxonase 2
1375857_at	similar to myoferlin (fer-1 like protein 3)
1375882_at	protein phosphatase 3, catalytic subunit, beta isoform

Supplemental Data Table S4. Continued.

1375921_at, 1393643_at	reticulocalbin (predicted)
1375928_at	similar to set domain-containing protein
1375928_at	similar to histone-lysine n-methyltransferase, h4 lysine-20 specific (histone h4-k20 methyltransferase) (h4-k20-hmtase) (set domain-containing protein 8) (pr/set domain-containing protein 07) (pr/set07) (pr-set7) (predicted)
1375956_at	menage a trois 1
1375964_at	phosphoserine phosphatase
1375970_at	,gb:ai010423 /db_xref=gi:3224255 /db_xref=est204874 /clone=rlubz28 /fea=est /cnt=9 /tid=rn.15886.1 /tier=consend /stk=5 /ug=rn.15886 /ug_title=ests
1375972_at	similar to membrane protein expressed in epithelial-like lung adenocarcinoma (predicted)
1375980_at	nucleoredoxin (predicted)
1375989_a_at	similar to nuclear factor kappa b subunit p100
1376005_at	kinesin family member 1b
1376010_at	prp4 pre-mrna processing factor 4 homolog b (yeast)
1376018_at	similar to lmnb2 protein
1376021_at	,gb:bm384049 /db_xref=gi:18184102 /db_xref=ui-r-dm1-ckb-m-16-0-ui.s1 /clone=ui-r-dm1-ckb-m-16-0-ui /fea=est /cnt=7 /tid=rn.23110.1 /tier=consend /stk=5 /ug=rn.23110 /ug_title=ests
1376025_at	hmt1 hnrnp methyltransferase-like 1 (s. cerevisiae)
1376029_at	rab2, member ras oncogene family-like
1376039_at	serine/threonine kinase 6
1376045_at	,gb:aw529960 /db_xref=gi:7172374 /db_xref=ui-r-c4-alc-c-10-0-ui.s1 /clone=ui-r-c4-alc-c-10-0-ui /fea=est /cnt=7 /tid=rn.38784.1 /tier=consend /stk=5 /ug=rn.38784 /ug_title=ests
1376056_at	similar to poly (adp-ribose) polymerase family, member 10
1376084_a_at	extra spindle poles like 1 (s. cerevisiae) (predicted)
1376109_at	,gb:bm387711 /db_xref=gi:18187764 /db_xref=ui-r-cn1-cjj-j-06-0-ui.s1 /clone=ui-r-cn1-cjj-j-06-0-ui /fea=est /cnt=6 /tid=rn.48053.1 /tier=consend /stk=5 /ug=rn.48053 /ug_title=ests
1376129_at	similar to vacuolar protein sorting 13c protein
1376144_at	similar to b aggressive lymphoma (predicted)
1376153_at	,gb:be102621 /db_xref=gi:8494720 /db_xref=ui-r-bt1-aqs-b-05-0-ui.s1 /clone=ui-r-bt1-aqs-b-05-0-ui /fea=est /cnt=6 /tid=rn.22233.1 /tier=consend /stk=5 /ug=rn.22233 /ug_title=ests
1376160_at	similar to avian reticuloendotheliosis viral (v-rel) oncogene related b
1376171_at	ubiquitin specific protease 11
1376198_at	adipocyte-specific adhesion molecule
1376219_at	atpase, class i, type 8b, member 2
1376262_at	udp-glucuronate decarboxylase 1
1376268_at	adp-ribosylation factor 6
1376272_s_at	aa926063gene
1376297_at	arrestin domain containing 1
1376336_at	mediator of rna polymerase ii transcription, subunit 6 homolog (yeast) (predicted)
1376346_at	tnf receptor associated factor 4 (predicted)
1376481_at	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 9 (predicted)
1376570_at	chaperonin subunit 5 (epsilon)

Supplemental Data Table S4. Continued.

1376584_at	,gb:be116408 /db_xref=gi:8508513 /db_xref=ui-r-bs1-ayc-h-09-0-ui.s1 /clone=ui-r-bs1-ayc-h-09-0-ui /fea=est /cnt=12 /tid=rn.27685.1 /tier=consend /stk=4 /ug=rn.27685 /ug_title=ests
1376596_at	dead (asp-glu-ala-asp) box polypeptide 42 (predicted)
1376610_a_at	similar to otthump00000028696
1376640_at	similar to hypothetical protein (predicted)
1376658_at	ras association (ralgds/af-6) and pleckstrin homology domains 1 (predicted)
1376669_at	,gb:bf283340 /db_xref=gi:11214410 /db_xref=est447931 /clone=rgiea65 /fea=est /cnt=9 /tid=rn.20857.1 /tier=consend /stk=4 /ug=rn.20857 /ug_title=ests
1376685_at	,gb:aw532489 /db_xref=gi:7174903 /db_xref=ui-r-bs0-ami-c-10-0-ui.s1 /clone=ui-r-bs0-ami-c-10-0-ui /fea=est /cnt=7 /tid=rn.40821.1 /tier=consend /stk=4 /ug=rn.40821 /ug_title=ests
1376722_at	nucleoporin 205kda (predicted)
1376737_at	similar to sumo/sentrin specific protease 5
1376771_at	,gb:bf412303 /db_xref=gi:11400292 /db_xref=ui-r-bt1-bnc-a-04-0-ui.s1 /clone=ui-r-bt1-bnc-a-04-0-ui /fea=est /cnt=6 /tid=rn.39269.1 /tier=consend /stk=4 /ug=rn.39269 /ug_title=ests
1376816_at	breast cancer 1
1376835_at	solute carrier family 35, member b2
1376877_at	,gb:aa893164 /db_xref=gi:3020043 /db_xref=est196967 /clone=rkibd01 /fea=est /cnt=7 /tid=rn.7729.1 /tier=consend /stk=4 /ug=rn.7729 /ug_title=ests
1377005_at	similar to cullin 4b
1377092_at	,gb:bf389682 /db_xref=gi:11374517 /db_xref=ui-r-bs2-bdn-e-06-0-ui.s1 /clone=ui-r-bs2-bdn-e-06-0-ui /fea=est /cnt=5 /tid=rn.41848.1 /tier=consend /stk=4 /ug=rn.41848 /ug_title=ests
1377103_at	,gb:aw525765 /db_xref=gi:7168150 /db_xref=ui-r-bj0p-air-e-10-0-ui.s1 /clone=ui-r-bj0p-air-e-10-0-ui /fea=est /cnt=5 /tid=rn.19310.1 /tier=consend /stk=4 /ug=rn.19310 /ug_title=ests
1377130_at	,gb:aw526352 /db_xref=gi:7168737 /db_xref=ui-r-bo1-ajb-b-08-0-ui.s1 /clone=ui-r-bo1-ajb-b-08-0-ui /fea=est /cnt=5 /tid=rn.7919.1 /tier=consend /stk=4 /ug=rn.7919 /ug_title=ests
1377151_at	,gb:ai102833 /db_xref=gi:4134123 /db_xref=est212122 /clone=rembt47 /fea=est /cnt=6 /tid=rn.22330.1 /tier=consend /stk=4 /ug=rn.22330 /ug_title=ests
1377379_at, 1386568_at	interferon regulatory factor 6 (predicted)
1377616_at	similar to riken cdna 6720467c03 (predicted)
1377651_at	triple functional domain (ptprf interacting)
1377753_at	,gb:bi295763 /db_xref=gi:14959536 /db_xref=ui-r-dk0-cfa-d-01-0-ui.s1 /clone=ui-r-dk0-cfa-d-01-0-ui /fea=est /cnt=6 /tid=rn.14853.1 /tier=consend /stk=3 /ug=rn.14853 /ug_title=ests
1377832_at	polo-like kinase 4 (drosophila) (predicted)
1379443_at	hermansky-pudlak syndrome 3 (predicted)
1379479_at	kinesin family member 4
1379497_at	,gb:bi275261 /db_xref=gi:14886936 /db_xref=ui-r-cx0-bwr-d-11-0-ui.s1 /clone=ui-r-cx0-bwr-d-11-0-ui /fea=est /cnt=5 /tid=rn.24928.1 /tier=consend /stk=2 /ug=rn.24928 /ug_title=ests
1379550_a_at	general transcription factor ii i repeat domain-containing 1
1382345_at	elk3, member of ets oncogene family (predicted)
1383051_at	synaptotagmin binding, cytoplasmic rna interacting protein

Supplemental Data Table S4. Continued.

1383175_a_at, 1392938_s_at, 1385458_a_at	similar to c11orf17 protein (predicted)
1383222_at	ferm-domain-containing protein 163scii
1383251_at	adp-ribosyltransferase (nad+, poly(adp-ribose) polymerase)-like 2 (predicted)
1383684_at	asf1 anti-silencing function 1 homolog b (s. cerevisiae) (predicted)
1383912_at	headcase homolog (drosophila) (predicted)
1383949_at	,gb:ai703880 /db_xref=gi:4991780 /db_xref=ui-r-ab1-yy-f-05-0-ui.s1 /clone=ui-r-ab1-yy-f-05-0-ui /fea=est /cnt=4 /tid=rn.41407.1 /tier=consend /stk=0 /ug=rn.41407 /ug_title=ests
1384548_at	ribosomal protein l32
1385236_at	similar to riken cdna 4931408l03 (predicted)
1386858_at, 1398872_at	ribosomal protein l13
1386859_at	transketolase
1386860_at	milk fat globule-egf factor 8 protein
1386861_at	h2a histone family, member z
1386862_at	annexin a5
1386863_at	protein phosphatase 1, catalytic subunit, alpha isoform
1386866_at	tyrosine 3-monooxgenase/tryptophan 5-monooxgenase activation protein, gamma polypeptide
1386868_at	ribosomal protein s10
1386874_at	ribosomal protein s15
1386879_at	lectin, galactose binding, soluble 3
1386882_at	t-complex testis expressed 1
1386888_at	eukaryotic translation initiation factor 4e binding protein 1
1386890_at	s100 calcium binding protein a10 (calpactin)
1386893_at	granulin
1386895_at	melanoma antigen, family d, 1
1386896_at, 1398773_at	src associated in mitosis, 68 kda
1386897_at	heterogeneous nuclear ribonucleoproteins methyltransferase-like 2 (s. cerevisiae)
1386910_a_at	apurinic/apyrimidinic endonuclease 1
1386912_at	procollagen c-proteinase enhancer protein
1386913_at	glycoprotein 38
1386925_at	actin related protein 2/3 complex, subunit 1b
1386926_at	acyl-coa synthetase long-chain family member 5
1386940_at	tissue inhibitor of metalloproteinase 2
1386941_at	plectin 1
1386945_a_at	protein kinase, amp-activated, beta 1 non-catalytic subunit
1386956_at	scavenger receptor class b, member 1
1386976_at	kangai 1
1386981_at	solute carrier family 16 (monocarboxylic acid transporters), member 1
1386984_at	mad homolog 4 (drosophila)
1386985_at	glutathione s-transferase, mu 1
1386996_at, 1388114_at	myosin light chain, regulatory b

Supplemental Data Table S4. Continued.

1386999_at, 1398800_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide
1387015_at	profilin 2
1387024_at	dual specificity phosphatase 6
1387027_a_at	lectin, galactose binding, soluble 9
1387048_at	nuclear rna helicase, decd variant of dead box family
1387060_at, 1388986_at	core promoter element binding protein
1387062_a_at	checkpoint kinase 1 homolog (s. pombe)
1387080_at	chondroitin sulfate proteoglycan 6
1387081_at	reticulocalbin 2
1387108_at	casein kinase 2, beta subunit
1387120_at	proteasome (prosome, macropain) 26s subunit, atpase 3
1387144_at	integrin alpha 1
1387262_at	sjogren syndrome antigen b
1387273_at	interleukin 1 receptor-like 1
1387280_a_at	tumor-associated protein 1
1387343_at	ccaat/enhancer binding protein (c/ebp), delta
1387345_at	proteasome (prosome, macropain) activator subunit 4
1387346_at, 1368819_at	integrin beta 1 (fibronectin receptor beta)
1387605_at	caspase 12
1387774_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
1387798_a_at	complement receptor related protein
1387802_at	discs, large (drosophila) homolog-associated protein 1
1387806_at	ras related protein 1b
1387818_at	caspase 11
1387871_at	cofilin 1
1387883_a_at	thymosin, beta 4
1387884_at	proteasome (prosome, macropain) subunit, alpha type 5
1387887_at	ribosomal protein l14
1387888_at	ribosomal protein s9
1387897_at	cyclic nucleotide phosphodiesterase 1
1387908_at	ras, dexamethasone-induced 1
1387909_at	hypothetical loc301448
1387946_at	lectin, galactoside-binding, soluble, 3 binding protein
1387965_at	kidney injury molecule 1
1387995_a_at	interferon-inducible protein variant 10
1388119_at	similar to hnrpa3 protein
1388119_at	hypothetical gene supported by y16641
1388119_at	similar to hnrpa3 protein
1388134_at	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
1388143_at, 1388459_at	collagen, type xviii, alpha 1
1388154_at	e2f transcription factor 5
1388158_at	hla-b-associated transcript 1a
1388170_at	vitamin a-deficient testicular protein 5

Supplemental Data Table S4. Continued.

1388297_at	eukaryotic translation elongation factor 1 gamma
1388303_at	ribosomal protein l26
1388309_at	high mobility group at-hook 1
1388314_at	high mobility group nucleosomal binding domain 1
1388333_at	ring-box 1
1388335_at	transgelin 2
1388340_at	ns5a (hepatitis c virus) transactivated protein 9
1388345_at	p21 (cdkn1a)-activated kinase 2
1388356_at	s100 calcium binding protein a16 (predicted)
1388369_at	similar to gp25l2 protein
1388377_at	coatomer protein complex subunit alpha
1388378_at	eukaryotic translation initiation factor 3, subunit 8, 110kda
1388381_at	eukaryotic translation initiation factor 3, subunit 4 (delta)
1388389_at	septin 2
1388392_at	tax1 (human t-cell leukemia virus type i) binding protein 3
1388393_at	proteolipid protein 2 (mapped)
1388397_at	ebna1 binding protein 2
1388408_at	similar to riken cdna 1110020c13
1388413_at	ribosome binding protein 1 homolog 180kda (dog) (predicted)
1388425_at	similar to riken cdna d130038b21
1388427_at	limitrin
1388436_at	small nuclear ribonucleoprotein polypeptide a
1388440_at	presenilin stabilization factor-like
1388443_at	cdk2 (cyclin-dependent kinase 2)-associated protein 1 (predicted)
1388446_at	similar to heterogeneous nuclear ribonucleoprotein a0
1388447_at	,gb:aa800701 /db_xref=gi:4131531 /db_xref=est190198 /clone=rluak44 /fea=est /cnt=27 /tid=rn.37644.1 /tier=stack /stk=17 /ug=rn.37644 /ug_title=ests
1388455_at	guanine nucleotide binding protein (g protein), gamma 10
1388458_at	replication factor c (activator 1) 4 (predicted)
1388460_at	capping protein (actin filament), gelsolin-like
1388464_at	cullin 7 (predicted)
1388468_at	similar to small protein effector 1 of cdc42
1388476_at	tial1 cytotoxic granule-associated rna binding protein-like 1 (mapped)
1388477_at	similar to ran-binding protein 3 (ranbp3)
1388478_at	,gb:be108225 /db_xref=gi:8500330 /db_xref=ui-r-bs1-ayw-h-02-0-ui.s1 /clone=ui-r-bs1-ayw-h-02-0-ui /fea=est /cnt=17 /tid=rn.34428.1 /tier=stack /stk=17 /ug=rn.34428 /ug_title=ests
1388479_at	dihydropyrimidinase-like 3
1388481_at	ribosomal protein s28
1388482_at	similar to riken cdna 9130404d14
1388484_at	ubiquitin-conjugating enzyme e2c (predicted)
1388488_at	lsm3 homolog, u6 small nuclear rna associated (s. cerevisiae) (predicted)
1388494_at	procollagen, type iv, alpha 2 (predicted)
1388505_at	,gb:be109642 /db_xref=gi:8501747 /db_xref=ui-r-bj1-avq-e-04-0-ui.s1 /clone=ui-r-bj1-avq-e-04-0-ui /fea=est /cnt=20 /tid=rn.2378.1 /tier=stack /stk=16 /ug=rn.2378 /ug_title=ests
1388514_at	protein phosphatase 1g (formerly 2c), magnesium-dependent, gamma isoform

Supplemental Data Table S4. Continued.

1388524_at	,gb:bf284328 /db_xref=gi:11215398 /db_xref=est448919 /clone=rgieo40 /fea=est /cnt=18 /tid=rn.9323.1 /tier=stack /stk=15 /ug=rn.9323 /ug_title=ests
1388528_at	fibrillarin
1388557_at	complement component 7 (predicted)
1388565_at	spastic paraplegia 21 homolog (human)
1388568_at	eukaryotic translation initiation factor 3 subunit 7
1388581_at	hematological and neurological expressed sequence 1
1388587_at	immediate early response 3
1388594_at	cysteine-rich with egf-like domains 1
1388600_at	similar to putative membrane steroid receptor
1388618_at	nidogen 2
1388622_at	nucleolar protein 5a
1388625_at	similar to riken cdna 4921521j11 (predicted)
1388628_at	integral type i protein
1388629_at	inosine 5-monophosphate dehydrogenase 2
1388645_at	similar to riken cdna 2810409h07
1388650_at	topoisomerase (dna) 2 alpha
1388682_at	cornichon homolog (drosophila) (predicted)
1388704_at	loc499834
1388711_at	interleukin 13 receptor, alpha 1
1388716_at	euchromatic histone lysine n-methyltransferase 2
1388717_at	protein o-fucosyltransferase 2 (predicted)
1388728_at	lysosomal-associated protein transmembrane 4b
1388729_at	harvey rat sarcoma oncogene, subgroup r (predicted)
1388745_at	sema domain, immunoglobulin domain (ig), transmembrane domain (tm) and short cytoplasmic domain, (semaphorin) 4a
1388759_at	chloride intracellular channel 4
1388761_at	histone deacetylase 1 (predicted)
1388763_at	similar to h2-calponin
1388767_at	programmed cell death 6 (predicted)
1388776_at	scotin
1388777_at	signal sequence receptor, gamma
1388785_at	dynein, axonemal, light chain 4
1388794_at	rna binding motif protein, x chromosome retrogene (predicted)
1388827_at	h2a histone family, member v (predicted)
1388827_at	similar to h2a histone family, member v isoform 1
1388840_at	similar to common-site lymphoma/leukemia gef (predicted)
1388865_at	protein phosphatase 4, regulatory subunit 2 (predicted)
1388867_at	similar to transcription factor
1388868_at	zinc finger protein 216 (predicted)
1388871_at	ash2 (absent, small, or homeotic)-like (drosophila) (predicted)
1388882_at	fk506 binding protein 3 (predicted)
1388897_at	wd repeat domain 5
1388900_at	hypothetical loc361797
1388902_at	lysyl oxidase-like 1
1388906_at	similar to novel protein similar to tensin tns
1388930_at	similar to riken cdna 2310075c12
1388932_at	laminin, alpha 5

Supplemental Data Table S4. Continued.

1388943_at	chromatin accessibility complex 1 (predicted)
1388959_at	similar to kiaa0153 protein (predicted)
1388974_at	signal recognition particle 19 (predicted)
1388992_at	e1a binding protein p400
1388997_at	adp-ribosylation factor 3
1389010_at	leukotriene a4 hydrolase
1389031_at	similar to coatomer gamma-2 subunit (gamma-2 coat protein) (gamma-2 cop)
1389052_at	tetratricopeptide repeat domain 13
1389063_at	exportin 6
1389087_at	anaphase promoting complex subunit 2
1389088_at	activity-dependent neuroprotective protein
1389103_at	similar to riken cdna 2810037c03
1389110_at	similar to mitochondrial ribosomal protein s6
1389145_at	cdc42 effector protein (rho gtpase binding) 2
1389165_at	similar to myocardial ischemic preconditioning upregulated protein 2
1389187_at	similar to riken cdna 1700088e04; dna segment, human est j0827e04; mus est j0827e04; dna segment, est j0827e04
1389189_at, 1398294_at	actinin, alpha 1
1389191_at	similar to riken cdna 2210415m20 (predicted)
1389193_at	,gb:bm388083 /db_xref=gi:18188136 /db_xref=ui-r-dm1-cjz-d-11-0-ui.s1 /clone=ui-r-dm1-cjz-d-11-0-ui /fea=est /cnt=10 /tid=rn.41133.1 /tier=stack /stk=8 /ug=rn.41133 /ug_title=ests
1389197_at	similar to riken cdna 9630046k23
1389209_at	similar to hypothetical protein bc002942
1389210_at	lymphocyte cytosolic protein 1
1389220_at	,gb:be112918 /db_xref=gi:8505023 /db_xref=ui-r-bj1-awa-d-03-0-ui.s1 /clone=ui-r-bj1-awa-d-03-0-ui /fea=est /cnt=9 /tid=rn.30073.1 /tier=stack /stk=8 /ug=rn.30073 /ug_title=ests
1389222_at	tryptophan hydroxylase 1
1389228_at	similar to riken cdna 2010309e21 (predicted)
1389246_at	,gb:bf282414 /db_xref=gi:11213396 /db_xref=est446917 /clone=rgidm31 /fea=est /cnt=9 /tid=rn.8685.1 /tier=stack /stk=8 /ug=rn.8685 /ug_title=ests
1389263_at	retinoic acid induced 14
1389281_at	similar to ankyrin repeat domain 25
1389282_at	integrin alpha 3 (predicted)
1389289_at	ewing sarcoma breakpoint region 1
1389293_at	cleavage and polyadenylation specific factor 2 (predicted)
1389294_at	cytoplasmic fmr1 interacting protein 1 (predicted)
1389304_at	re1-silencing transcription factor
1389326_at	replication factor c (activator 1) 3
1389351_at	similar to fli-lrr associated protein-1
1389355_at	immediate early response 5
1389373_at	mad homolog 1 (drosophila)
1389385_at	endothelial precursor protein b9 (predicted)
1389394_at	,gb:ai411809 /db_xref=gi:4255313 /db_xref=est240103 /clone=rkidn14 /fea=est /cnt=10 /tid=rn.23552.1 /tier=stack /stk=7 /ug=rn.23552 /ug_title=ests
1389395_at	selenoprotein n, 1 (predicted)
1389408_at	ribonucleotide reductase m2 (mapped)

Supplemental Data Table S4. Continued.

1389409_at	similar to testis derived transcript
1389420_at	signal-transducing adaptor protein-2
1389435_at	,gb:be329046 /db_xref=gi:9202822 /db_xref=hq36a12.x1 /clone=image:3121438 /fea=est /cnt=8 /tid=rn.25342.1 /tier=stack /stk=7 /ug=rn.25342 /ug_title=ests
1389440_at	similar to cell division cycle associated 5
1389454_at	programmed cell death 5 (predicted)
1389463_at	protein kinase, camp dependent regulatory, type i, beta
1389485_at	similar to transformed mouse 3t3 cell double minute 1
1389494_at	ribosomal protein s6 kinase, polypeptide 4 (predicted)
1389518_at	f-box only protein 10 (predicted)
1389520_at	similar to wdr1 protein
1389534_at	ubiquitin-conjugating enzyme e2e 3, ubc4/5 homolog (yeast) (predicted)
1389555_at	transcription factor 19
1389566_at	cyclin b2
1389580_at	loc499580
1389617_at	nima (never in mitosis gene a)- related kinase 9 (predicted)
1389658_at	similar to cg6133-pa (predicted)
1389668_at	similar to ad024 protein
1389697_at	similar to otthump00000018288
1389697_at	,gb:aw529759 /db_xref=gi:7172173 /db_xref=ui-r-bu0-amt-a-02-0-ui.s1 /clone=ui-r-bu0-amt-a-02-0-ui /fea=est /cnt=7 /tid=rn.45060.1 /tier=stack /stk=6 /ug=rn.45060 /ug_title=ests
1389760_at	ring finger protein 134
1389815_at	protein phosphatase 1, regulatory (inhibitor) subunit 14b
1389857_at	similar to ww domain binding protein 5
1389873_at	apoptosis-associated speck-like protein containing a card
1389885_at	similar to riken cdna 0610025l06
1389966_at	procollagen, type vi, alpha 3 (predicted)
1389980_at	similar to protein hspc163
1390022_at	actin related protein 2/3 complex, subunit 5
1390058_at	similar to dkfzp547e1010 protein
1390082_at	huntingtin interacting protein 1
1390107_at	synaptotagmin-like 2 (predicted)
1390109_at	,gb:bi303073 /db_xref=gi:14979353 /db_xref=ui-r-dq0-ciz-a-05-0-ui.s1 /clone=ui-r-dq0-ciz-a-05-0-ui /fea=est /cnt=11 /tid=rn.25065.1 /tier=consend /stk=5 /ug=rn.25065 /ug_title=ests
1390116_at	polymerase i and transcript release factor (predicted)
1390133_at	bcl2/adenovirus e1b 19kda-interacting protein 1, nip2 (predicted)
1390137_at	traf4 associated factor 1
1390138_at	similar to coiled-coil domain containing 8
1390173_at	,gb:bg377886 /db_xref=gi:13302358 /db_xref=ui-r-cu0-bvg-d-03-0-ui.s1 /clone=ui-r-cu0-bvg-d-03-0-ui /fea=est /cnt=7 /tid=rn.9561.1 /tier=consend /stk=5 /ug=rn.9561 /ug_title=ests
1390177_at	,gb:ai233857 /db_xref=gi:3817737 /db_xref=est230545 /clone=rlucs05 /fea=est /cnt=9 /tid=rn.6397.1 /tier=consend /stk=5 /ug=rn.6397 /ug_title=ests
1390187_at	,gb:ai060043 /db_xref=gi:3333820 /db_xref=ui-r-c1-kz-c-08-0-ui.s1 /clone=ui-r-c1-kz-c-08-0-ui /fea=est /cnt=7 /tid=rn.19122.1 /tier=consend /stk=5 /ug=rn.19122 /ug_title=ests
1390214_a_at	cdkn1a interacting zinc finger protein 1 (predicted)

Supplemental Data Table S4. Continued.

1390226_at	similar to hypothetical protein loc340061
1390249_at	similar to dkfzp434h132 protein
1390278_at	similar to riken cdna g430041m01
1390383_at	adipose differentiation-related protein
1390384_at	similar to histone h2a.x (h2a/x)
1390386_at	caspase 3, apoptosis related cysteine protease
1390415_at	thyroid hormone receptor interactor 13
1390436_at	autophagy 7-like (s. cerevisiae)
1390459_at	,gb:bg670247 /db_xref=gi:13892346 /db_xref=drnacb12 /clone=drnacb12 /fea=est /cnt=6 /tid=rn.17961.1 /tier=consend /stk=4 /ug=rn.17961 /ug_title=ests
1390469_at	nurim (nuclear envelope membrane protein)
1390510_at	membrane-spanning 4-domains, subfamily a, member 6b
1390515_at	,gb:aa998383 /db_xref=gi:4289475 /db_xref=ui-r-c0-hz-g-04-0-ui.s1 /clone=ui-r-c0-hz-g-04-0-ui /fea=est /cnt=5 /tid=rn.13339.1 /tier=consend /stk=4 /ug=rn.13339 /ug_title=ests
1390582_s_at	neurotrophin receptor associated death domain
1390604_s_at	integrin beta 3 binding protein (beta3-endonexin)
1390650_at	pericentrin 1
1390692_at	cytidine 5'-triphosphate synthase (predicted)
1390947_at	similar to riken cdna d930036f22 gene
1391518_at	similar to 60s ribosomal protein l7a
1392467_at	inositol (myo)-1(or 4)-monophosphatase 2
1392900_at	similar to mkiaa1631 protein
1392926_at	laminin, alpha 1 (predicted)
1398304_at	frizzled homolog 2 (drosophila)
1398315_at	ribosomal protein l15
1398325_at	tetraspanin 3
1398347_at	axl receptor tyrosine kinase (predicted)
1398356_at	cleavage and polyadenylation specific factor 5
1398362_at	notch gene homolog 2 (drosophila)
1398373_at	udp-gal:betaglcnac beta 1,3-galactosyltransferase, polypeptide 3
1398425_at	similar to hypothetical protein mgc39325-like protein
1398442_at	similar to chromosome 14 open reading frame 80 (predicted)
1398749_at	ribosomal protein l4
1398751_at	similar to ribosomal protein s7
1398752_at	selenoprotein
1398756_at	similar to nucleophosmin (npm) (nucleolar phosphoprotein b23) (numatrin) (nucleolar protein no38)
1398756_at, 1399158_a_at, 1398757_at	nucleophosmin 1
1398759_at	transforming growth factor beta 1 induced transcript 4
1398760_at	ribosomal protein l35a
1398761_at	ribosomal protein l5
1398762_at	syndecan binding protein
1398765_at	adaptor-related protein complex 2, mu 1 subunit
1398766_at	ribophorin i
1398768_at	retinoblastoma binding protein 7

Supplemental Data Table S4. Continued.

1398774_at	ribosomal protein l30
1398775_at	ribosomal protein s15a
1398778_at	proteasome (prosome, macropain) subunit, alpha type 1
1398789_at	ribosomal protein l37
1398796_at	transmembrane trafficking protein 21
1398798_at	methionine aminopeptidase 2
1398801_at	cdk105 protein
1398803_at	dynein, cytoplasmic, heavy chain 1
1398806_at	phosphatidylinositol transfer protein
1398814_at	rab11a, member ras oncogene family
1398822_at	gdp dissociation inhibitor 2
1398827_at	cd 81 antigen
1398829_at	fk506 binding protein 1a
1398830_at	ribosomal protein l28
1398831_at	proteasome (prosome, macropain) subunit, beta type 4
1398832_at	nucleolin
1398836_s_at	actin, beta
1398850_at	peptidylprolyl isomerase a
1398851_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide
1398852_at	ribosomal protein s21
1398854_at	ribosomal protein l24
1398856_at	proteasome (prosome, macropain) subunit, alpha type 2
1398858_at	proteasome (prosome, macropain) 26s subunit, non-atpase, 2
1398871_at	ribosomal protein l17
1398872_at	ribosomal protein s13
1398877_at	stress-induced-phosphoprotein 1
1398882_at	ribosomal protein s5
1398885_at	ribosomal protein l23
1398886_at	similar to selenoprotein h
1398892_at	niemann pick type c2
1398897_at	ubiquitin-conjugating enzyme e2 variant 1 (predicted)
1398904_at	similar to nono protein
1398904_at	non-pou domain containing, octamer-binding
1398910_at	stip1 homology and u-box containing protein 1
1398913_at	nuclear mitotic apparatus protein 1
1398917_at	ribosomal protein l7
1398919_at	similar to hypothetical protein cgi-99
1398929_at	eukaryotic translation initiation factor 3, subunit 6 interacting protein
1398944_at	apoptotic chromatin condensation inducer 1
1398974_at	chromosome segregation 1-like (s. cerevisiae) (predicted)
1399020_at	similar to family with sequence similarity 40, member a
1399028_at	similar to riken cdna 5730454b08 (predicted)
1399033_at	core binding factor beta
1399053_at	,gb:bm391257 /db_xref=gi:18191310 /db_xref=ui-r-dy0-ckq-m-04-0-ui.s1 /clone=ui-r-dy0-ckq-m-04-0-ui /fea=est /cnt=9 /tid=rn.1096.1 /tier=stack /stk=8 /ug=rn.1096 /ug_title=ests
1399055_at	bromodomain containing 7 (predicted)
1399057_at	mortality factor 4 like 1

Supplemental Data Table S4. Continued.

1399088_at	tousled-like kinase 2 (arabidopsis) (predicted)
1399090_at	dynein, cytoplasmic, light intermediate chain 1
1399091_at	f-actin capping protein beta subunit
1399123_at	dead/h (asp-glu-ala-asp/his) box polypeptide 26
1399142_at	gle1 rna export mediator-like (yeast
1399143_at	ubiquitin-conjugating enzyme e2n
1399157_at	similar to nnx3 (predicted)
Down-Regulated Genes	
AFFY_ID	**Gene Name**
1367467_at	similar to nitrogen fixation cluster-like (predicted)
1367477_at	mitochondrial ribosomal protein l53 (predicted)
1367559_at	ferritin light chain 1
1367589_at	aconitase 2, mitochondrial
1367591_at	peroxiredoxin 3
1367609_at	macrophage migration inhibitory factor
1367619_at	progesterone receptor membrane component 1
1367629_at	cytochrome c oxidase, subunit viia 2
1367638_at	malonyl-coa decarboxylase
1367641_at	superoxide dismutase 1
1367653_a_at, 1372790_at	malate dehydrogenase 1, nad (soluble)
1367662_at	hydroxyacyl-coenzyme a dehydrogenase type ii
1367672_at	hydroxysteroid (17-beta) dehydrogenase 4
1367673_at	selenium binding protein 2
1367677_at	peroxiredoxin 5
1367680_at	acyl-coenzyme a oxidase 1, palmitoyl
1367695_at	quinoid dihydropteridine reductase
1367702_at	acetyl-coenzyme a dehydrogenase, medium chain
1367706_at	voltage-dependent anion channel 1
1367720_at	aminolevulinate, delta-, dehydratase
1367729_at	ornithine aminotransferase
1367741_at	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1
1367755_at	cysteine dioxygenase 1, cytosolic
1367767_at	3-hydroxy-3-methylglutaryl-coenzyme a lyase
1367774_at	glutathione s-transferase a3
1367775_at	alpha-methylacyl-coa racemase
1367793_at	d-dopachrome tautomerase
1367798_at	s-adenosylhomocysteine hydrolase
1367815_at	solute carrier family 5 (sodium-dependent vitamin transporter), member 6
1367828_at	acetyl-coenzyme a dehydrogenase, short chain
1367829_at	enoyl coenzyme a hydratase, short chain, 1, mitochondrial
1367838_at	ctl target antigen
1367839_at, 1389906_at	farnesyl diphosphate farnesyl transferase 1
1367843_at	aldo-keto reductase family 7, member a2 (aflatoxin aldehyde reductase)
1367845_at	neurofilament 3, medium
1367885_at	peroxisomal membrane protein 2
1367904_at	regulated endocrine-specific protein 18

Supplemental Data Table S4. Continued.

1367905_at	ectonucleotide pyrophosphatase/phosphodiesterase 3
1367908_at	glycine cleavage system protein h (aminomethyl carrier)
1367909_at	dicarbonyl l-xylulose reductase
1367917_at	cytochrome p450, family 2, subfamily d, polypeptide 26
1367937_at	hypothetical protein loc56728
1367952_at	low density lipoprotein receptor-related protein 2
1367953_at	tyro3 protein tyrosine kinase 3
1367988_at	cytochrome p450, family 2, subfamily c, polypeptide 23
1367994_at	dihydropyrimidine dehydrogenase
1367995_at	catalase
1367999_at	aldehyde dehydrogenase 2
1368008_at	prominin 1
1368038_at, 1368041_at	synaptojanin 2 binding protein
1368045_at, 1388534_at	solute carrier family 31 (copper transporters), member 1
1368047_at	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3
1368057_at	atp-binding cassette, sub-family d (ald), member 3
1368059_at	crystallin, mu
1368060_at	heat-responsive protein 12
1368077_at	fructose-1,6- biphosphatase 1
1368085_at	gtp cyclohydrolase i feedback regulator
1368091_at	5-oxoprolinase (atp-hydrolysing)
1368092_at	fumarylacetoacetate hydrolase
1368096_at	rab7, member ras oncogene family-like 1
1368121_at	aldo-keto reductase family 7, member a3 (aflatoxin aldehyde reductase)
1368137_at, 1387071_a_at	microtubule-associated protein tau
1368137_at, 1387071_a_at	hypothetical gene supported by nm_017212
1368139_s_at	alkaline phosphatase, tissue-nonspecific
1368150_at	solute carrier family 27 (fatty acid transporter), member 2
1368150_at	hypothetical gene supported by nm_031736
1368163_at, 1387084_at	dipeptidylpeptidase 4
1368164_at	biliverdin reductase a
1368178_at	pdz domain containing 1
1368180_s_at	glutathione-s-transferase, alpha type2
1368181_at	methylenetetrahydrofolate dehydrogenase (nadp+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthase
1368191_a_at	solute carrier family 22 (organic cation transporter), member 1
1368206_at	peroxisomal acyl-coa thioesterase 1
1368208_at	camello-like 1
1368209_at	membrane-associated protein 17
1368234_at	prolyl endopeptidase
1368236_at	meprin 1 alpha
1368245_at	ureidopropionase, beta
1368253_at	guanidinoacetate methyltransferase

Supplemental Data Table S4. Continued.

1368283_at	enoyl-coenzyme a, hydratase/3-hydroxyacyl coenzyme a dehydrogenase
1368288_at	group specific component
1368304_at	flavin containing monooxygenase 3
1368317_at	aquaporin 7
1368354_at	glutathione s-transferase theta 1
1368366_at	camello-like 2
1368372_at	steroid sulfatase
1368374_a_at	gamma-glutamyltransferase 1
1368378_at	formyltetrahydrofolate dehydrogenase
1368390_at	v-raf oncogene homolog 1 (murine sarcoma 3611 virus)
1368397_at	udp-glucuronosyltransferase 2 family, member 5
1368397_at	udp glycosyltransferase 2 family, polypeptide b4
1368399_a_at	plasma glutamate carboxypeptidase
1368409_at	glutathione s-transferase, theta 2
1368428_at	x-prolyl aminopeptidase (aminopeptidase p) 2, membrane-bound
1368431_at	hepsin
1368432_a_at	v-ros ur2 sarcoma virus oncogene homolog 1 (avian)
1368440_at	solute carrier family 3, member 1
1368442_at	coagulation factor 2
1368452_at	atp-binding cassette, sub-family c (cftr/mrp), member 6
1368460_at	solute carrier family 2, member 5
1368467_at	cytochrome p450, family 4, subfamily f, polypeptide 2
1368470_at	gamma-glutamyl hydrolase
1368498_a_at, 1387974_a_at	kidney specific organic anion transporter
1368509_at	bardet-biedl syndrome 2 (human)
1368512_a_at	glutamyl aminopeptidase
1368521_at	napsin a aspartic peptidase
1368552_at	grpe-like 1, mitochondrial
1368562_at	sulfotransferase family 4a, member 1
1368563_at	aspartoacylase
1368566_a_at	nadh dehydrogenase (ubiquinone) flavoprotein 3-like
1368575_at	solute carrier family 6 (neurotransmitter transporter), member 18
1368607_at, 1393894_at	cytochrome p450, 4a12
1368627_at	regucalcin
1368651_at	pyruvate kinase, liver and red blood cell
1368674_at	liver glycogen phosphorylase
1368680_a_at	solute carrier family 34 (sodium phosphate), member 1
1368774_a_at	espin
1368779_a_at	guanylate cyclase 1, soluble, beta 2
1368794_at	3-hydroxyanthranilate 3,4-dioxygenase
1368806_at	selenoprotein p, plasma, 1
1368852_at	dnaj-like protein
1368882_at	sialyltransferase 7c
1368915_at	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)
1368924_at, 1373803_a_at	growth hormone receptor
1369081_at	neuraminidase 1

Supplemental Data Table S4. Continued.

1369100_at	angiotensin/vasopressin receptor
1369169_at	solute carrier family 23 (nucleobase transporters), member 1
1369200_at	5 nucleotidase
1369259_at	deiodinase, iodothyronine, type i
1369286_at	protein c
1369289_at	hepatocyte nuclear factor 4, alpha
1369304_at	6-pyruvoyl-tetrahydropterin synthase
1369401_at	solute carrier family 21, member 13
1369407_at	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)
1369412_a_at	solute carrier family 19, member 1
1369450_at	integral membrane transport protein ust5r
1369491_at	d-amino acid oxidase
1369493_at	prolactin receptor
1369506_at	glial cells missing homolog 1 (drosophila)
1369531_at	sulfotransferase family, cytosolic, 1c, member 2
1369625_at, 1387651_at	aquaporin 1
1369636_at	sorbitol dehydrogenase
1369654_at	protein kinase, amp-activated, alpha 2 catalytic subunit
1369663_at	epoxide hydrolase 2, cytoplasmic
1369705_at	x transporter protein 3
1369728_at	germinal histone h4 gene
1369799_at	4-aminobutyrate aminotransferase
1369939_at, 1387773_at	cytochrome c, somatic
1369970_at	vesicle-associated membrane protein 8
1369986_at	hydroxyacyl glutathione hydrolase
1369989_at	pyridoxine 5'-phosphate oxidase
1370006_at	nadh dehydrogenase (ubiquinone) fe-s protein 6
1370009_at	apolipoprotein c-iii
1370026_at	crystallin, alpha b
1370036_at	sulfite oxidase
1370060_at	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11
1370067_at, 1370870_at	malic enzyme 1
1370072_at	membrane metallo endopeptidase
1370075_at	dihydrofolate reductase
1370144_at	similar to gtp-binding protein ngb
1370144_at	gtp binding protein 4
1370144_at, 1372869_at	similar to gtp-binding protein ngb
1370147_at	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase
1370163_at	ornithine decarboxylase 1
1370166_at, 1370167_at	syndecan 2
1370187_at	propionyl coenzyme a carboxylase, beta polypeptide
1370232_at	isovaleryl coenzyme a dehydrogenase
1370259_a_at	parathyroid hormone receptor 1

Supplemental Data Table S4. Continued.

1370275_at	atp synthase, h+ transporting, mitochondrial f1 complex, beta polypeptide
1370276_at	atp synthase, h+ transporting, mitochondrial f1 complex, o subunit
1370281_at	fatty acid binding protein 5, epidermal
1370296_at, 1387896_at	sterol carrier protein 2
1370299_at	aldolase b
1370320_at	mawd binding protein
1370329_at, 1387913_at	cytochrome p450, family 2, subfamily d, polypeptide 22
1370336_at	pregnancy-induced growth inhibitor
1370361_at	cell growth regulator with ef hand domain 1
1370362_at	protein tyrosine phosphatase, receptor type, n
1370363_at	carboxylesterase 3
1370365_at	glutathione synthetase
1370367_at, 1387932_at	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system xag), member 1
1370377_at	cytochrome p450, family 2, subfamily d, polypeptide 10
1370377_at	cytochrome p450, family 2, subfamily d, polypeptide 9
1370378_at	atp synthase, h+ transporting, mitochondrial f1 complex, alpha subunit, isoform 1
1370379_at	protease, serine, 8 (prostasin)
1370385_at, 1377408_at, 1387941_s_at	phospholipase a2, group vi
1370397_at	cytochrome p450, family 4, subfamily a, polypeptide 14
1370446_at	non-metastatic cells 7, protein expressed in
1370474_at	thyroid hormone receptor beta
1370509_at	pyruvate dehydrogenase phosphatase isoenzyme 2
1370547_at	pregnancy-zone protein
1370688_at, 1372523_at	glutamate-cysteine ligase, catalytic subunit
1370699_a_at	peptidase d (mapped)
1370699_a_at	epidermal growth factor receptor
1370806_at	all-trans-13,14-dihydroretinol saturase
1370814_at	dehydrogenase/reductase (sdr family) member 4
1370818_at	2-4-dienoyl-coenzyme a reductase 2, peroxisomal
1370821_at	thiopurine methyltransferase
1370824_at	solute carrier family 38, member 3
1370853_at, 1374307_at	calcium/calmodulin-dependent protein kinase ii inhibitor 1
1370861_at	cytochrome c oxidase, subunit via, polypeptide 1
1370865_at	isocitrate dehydrogenase 3, gamma
1370879_at	afadin
1370881_at	thiosulfate sulfurtransferase
1370897_at	branched chain ketoacid dehydrogenase e1, alpha polypeptide
1370906_at	branched chain keto acid dehydrogenase e1, beta polypeptide
1370907_at	sialyltransferase 1
1370918_a_at	atp synthase, h+ transporting, mitochondrial f1 complex, gamma polypeptide 1

Supplemental Data Table S4. Continued.

1370929_at, 1388148_a_at	low density lipoprotein receptor-related protein associated protein 1
1370936_at	dimethylglycine dehydrogenase precursor
1370943_at	sulfotransferase family, cytosolic, 1c, member 1 (predicted)
1370964_at	argininosuccinate synthetase
1371008_at	peptidase (mitochondrial processing) alpha
1371012_at	2-hydroxyphytanoyl-coenzyme a lyase
1371041_at	nadh dehydrogenase (ubiquinone) flavoprotein 2
1371150_at	cyclin d1
1371253_at	electron transferring flavoprotein, alpha polypeptide
1371266_at	afamin
1371296_at, 1388294_at	succinate dehydrogenase complex, subunit d, integral membrane protein
1371309_at	testis enhanced gene transcript
1371312_at	coiled-coil-helix-coiled-coil-helix domain containing 2
1371346_at	nadh dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kda (predicted)
1371350_at	similar to s-adenosylmethionine synthetase gamma form (methionine adenosyltransferase) (adomet synthetase) (mat-ii)
1371360_at	n-myc downstream regulated gene 1
1371363_at	glycerol-3-phosphate dehydrogenase 1 (soluble)
1371379_at	similar to brain protein 44
1371380_at	pyruvate dehydrogenase e1 alpha 1
1371381_at	similar to tbc1 domain family member 4
1371388_at	pyruvate dehydrogenase (lipoamide) beta
1371389_at	hypothetical loc306766
1371398_at	,gb:bf281400 /db_xref=gi:11212470 /db_xref=est445991 /clone=rgiae29 /fea=est /cnt=44 /tid=rn.3543.1 /tier=stack /stk=27 /ug=rn.3543 /ug_title=ests, highly similar to atpk mouse atp synthase f chain, mitochondrial (m.musculus)
1371405_at	similar to hypothetical protein mgc52110
1371416_at	nadh dehydrogenase (ubiquinone) flavoprotein 1, 51kda
1371420_at	92aa-protein
1371421_at	similar to flj40243 protein (predicted)
1371431_at	peroxisome biogenesis factor 5 (predicted)
1371448_at	,gb:ai599295 /db_xref=gi:4608343 /db_xref=est250998 /clone=remeq51 /fea=est /cnt=27 /tid=rn.11514.1 /tier=stack /stk=24 /ug=rn.11514 /ug_title=ests
1371456_at	atp-binding cassette, sub-family f (gcn20), member 3
1371482_at	nadh dehydrogenase (ubiquinone) fe-s protein 2
1371496_at	,gb:ai178804 /db_xref=gi:3729442 /db_xref=est222486 /clone=rspbm81 /fea=est /cnt=23 /tid=rn.13458.1 /tier=stack /stk=22 /ug=rn.13458 /ug_title=ests
1371548_at	mitochondrial ribosomal protein s25
1371549_at	wd repeat domain 23
1371553_at	mitochondrial ribosomal protein l36 (predicted)
1371567_at	aldehyde dehydrogenase family 7, member a1
1371599_at	lrrgt00097
1371608_at	mitochondrial ribosomal protein s34 (predicted)
1371609_at	homolog of zebrafish es1
1371615_at	diacylglycerol o-acyltransferase homolog 2 (mouse)

Supplemental Data Table S4. Continued.

1371661_at	mitochondrial ribosomal protein s23 (predicted)
1371680_at	gamma-aminobutyric acid (gaba(a)) receptor-associated protein-like 1 (predicted)
1371701_at	nadh dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (predicted)
1371729_at, 1373826_at	yippee-like 5 (drosophila)
1371730_at	similar to riken cdna 1300002a08
1371739_at, 1375289_at	leucine zipper-ef-hand containing transmembrane protein 1
1371762_at	retinol binding protein 4, plasma
1371763_at	similar to riken cdna 4931406c07
1371773_at	,gb:ai179413 /db_xref=gi:3730051 /db_xref=est223117 /clone=rspcg95 /fea=est /cnt=21 /tid=rn.22153.1 /tier=stack /stk=16 /ug=rn.22153 /ug_title=ests
1371775_at	acyl-coenzyme a dehydrogenase, short/branched chain
1371783_at	heat shock protein
1371789_at	similar to clpp protease
1371811_at	bernardinelli-seip congenital lipodystrophy 2 homolog (human)
1371818_at	exportin, trna (nuclear export receptor for trnas) (predicted)
1371824_at	adenylate kinase 3-like 1
1371833_at	brain protein i3
1371886_at	carnitine acetyltransferase
1371894_at	glucosamine (n-acetyl)-6-sulfatase
1371912_at	nadh dehydrogenase (ubiquinone) fe-s protein 7
1371913_at	transforming growth factor, beta induced
1371916_at	selenoprotein x 1 (predicted)
1371922_at	,gb:ai169140 /db_xref=gi:4134369 /db_xref=est214974 /clone=rkibo03 /fea=est /cnt=17 /tid=rn.18638.1 /tier=stack /stk=15 /ug=rn.18638 /ug_title=ests
1371942_at	similar to glutathione s-transferase, theta 3
1371959_at	similar to hist2h2aa1 protein
1371959_at	histone 2, h2aa (predicted)
1371963_at	propionyl-coenzyme a carboxylase, alpha polypeptide
1371965_at	similar to riken cdna 2010311d03
1371974_at	phytanoyl-coa dioxygenase domain containing 1
1371986_at	acidic (leucine-rich) nuclear phosphoprotein 32 family, member a
1372076_at	hepatitis b virus x interacting protein (predicted)
1372087_at	hypertrophic agonist responsive protein b64
1372098_at	similar to hypothetical protein mgc14141
1372103_at, 1398343_at	dnaj (hsp40) homolog, subfamily a, member 4
1372123_at	succinate dehydrogenase complex, subunit b, iron sulfur (ip) (predicted)
1372132_at	cndp dipeptidase 2 (metallopeptidase m20 family)
1372149_at	au rna binding protein/enoyl-coenzyme a hydratase (predicted)
1372150_at	ubiquitin specific protease 10
1372157_at	similar to cgi-143 protein (predicted)
1372158_at	lrp16 protein
1372170_at	aminoacylase 1
1372175_at	,gb:be112899 /db_xref=gi:8505004 /db_xref=ui-r-bj1-awa-b-06-0-ui.s1 /clone=ui-r-bj1-awa-b-06-0-ui /fea=est /cnt=15 /tid=rn.1132.1 /tier=stack

Supplemental Data Table S4. Continued.

	/stk=13 /ug=rn.1132 /ug_title=ests
1372177_at	molybdopterin synthase
1372199_at, 1372475_at	pten induced putative kinase 1 (predicted)
1372205_at	zinc finger protein 278
1372208_at	protein phosphatase 1, regulatory (inhibitor) subunit 1b
1372227_at	muted (predicted)
1372245_at	wd40 protein ciao1
1372254_at	serine (or cysteine) peptidase inhibitor, clade g, member 1
1372261_at	,gb:ai409067 /db_xref=gi:4252571 /db_xref=est237359 /clone=rkido56 /fea=est /cnt=17 /tid=rn.3650.1 /tier=stack /stk=12 /ug=rn.3650 /ug_title=ests
1372277_at	taste receptor, type 1, member 2
1372297_at	glutathione s-transferase, alpha 4
1372306_at	ethylmalonic encephalopathy 1 (predicted)
1372310_at	similar to tumor-related protein
1372323_at	sarcosine dehydrogenase
1372358_at, 1389540_at	tg interacting factor
1372372_at	similar to ab2-225
1372395_at	similar to kiaa0597 protein
1372422_at, 1389833_at	sulfatase modifying factor 1 (predicted)
1372437_at	s-phase kinase-associated protein 1a
1372438_at	similar to nit protein 2
1372485_at	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (tcf1) 1
1372498_at	similar to riken cdna 2810413n20
1372554_at	similar to rw1 protein (predicted)
1372592_at	histone deacetylase 6
1372600_at	similar to f-box only protein 31
1372612_at	dynein light chain-2
1372613_at	dehydrogenase/reductase (sdr family) member 6 (predicted)
1372637_at	,gb:ai169241 /db_xref=gi:3705549 /db_xref=est215076 /clone=rkibp21 /fea=est /cnt=12 /tid=rn.14890.1 /tier=stack /stk=11 /ug=rn.14890 /ug_title=ests, weakly similar to pn0109 keratin-like protein - rat (r.norvegicus)
1372654_at	eps8-like 2 (predicted)
1372655_at	,gb:bg380323 /db_xref=gi:13304795 /db_xref=ui-r-cs0-btv-g-05-0-ui.s1 /clone=ui-r-cs0-btv-g-05-0-ui /fea=est /cnt=12 /tid=rn.14791.1 /tier=stack /stk=11 /ug=rn.14791 /ug_title=ests
1372670_at	similar to hypothetical protein flj21827
1372672_at	quinolinate phosphoribosyltransferase
1372676_at	similar to riken cdna 1110025h10
1372715_at	sideroflexin 1
1372734_at	small cell adhesion glycoprotein
1372741_at	similar to riken cdna c330023f11
1372744_at	plakophilin 4 (predicted)
1372765_a_at	peroxisomal delta3, delta2-enoyl-coenzyme a isomerase

Supplemental Data Table S4. Continued.

1372765_a_at, 1388884_at	similar to riken cdna 1810022c23
1372774_at	coenzyme q6 homolog (yeast)
1372780_at	similar to riken cdna 1110038m16 (predicted)
1372794_at	death-associated kinase 2
1372841_at	deleted in polyposis 1-like 1
1372847_at	acn9 homolog (s. cerevisiae)
1372860_at	similar to phospholysine phosphohistidine inorganic pyrophosphate phosphata (5m590)
1372866_at	similar to hypothetical protein mgc18873
1372876_at	selenophosphate synthetase 2
1372895_at	similar to riken cdna 5730469m10
1372907_at	atpase, h+ transporting, v0 subunit e isoform 2
1372908_at	t-complex expressed gene 1 (predicted)
1372942_at	exosome component 5 (predicted)
1372976_at	similar to dorz1
1372985_at	zinc finger protein 444 (predicted)
1372996_at	similar to riken cdna 0610042e07
1373020_at	similar to mitochondria-associated granulocyte macrophage csf signaling molecule
1373110_at	,gb:ai407487 /db_xref=gi:4250991 /db_xref=est235776 /clone=rovdu14 /fea=est /cnt=13 /tid=rn.1452.1 /tier=stack /stk=9 /ug=rn.1452 /ug_title=ests
1373134_at	similar to riken cdna b430104h02
1373180_at	,gb:ai227919 /db_xref=gi:3811806 /db_xref=est224614 /clone=rbrcn61 /fea=est /cnt=11 /tid=rn.17029.1 /tier=stack /stk=9 /ug=rn.17029 /ug_title=ests
1373182_at	,gb:bf281899 /db_xref=gi:11212969 /db_xref=est446490 /clone=rgibh79 /fea=est /cnt=11 /tid=rn.18416.1 /tier=stack /stk=9 /ug=rn.18416 /ug_title=ests
1373198_at	similar to riken cdna 2810451a06
1373218_at	similar to 6430514l14rik protein (predicted)
1373230_at	similar to cdna sequence bc036718
1373253_at	acyl-coenzyme a binding domain containing 4
1373277_at	similar to bbp-like protein 2
1373335_at	membrane-associated dhhc9 zinc finger protein
1373337_at	glyoxylate reductase/hydroxypyruvate reductase (predicted)
1373365_at	similar to ump-cmp kinase
1373371_a_at	similar to riken cdna 1110001j03
1373377_at	sodium channel modifier 1 (predicted)
1373386_at	gap junction channel protein connexin 26
1373400_at	protein kinase, camp-dependent, regulatory, type 2, alpha
1373411_at	similar to translation factor sui1 homolog (predicted)
1373420_at	evolutionarily conserved signaling intermediate in toll pathway
1373425_at	similar to cdc-like kinase 2
1373431_at	leucine-rich repeat-containing 5
1373518_at	similar to udp-n-acetylglucosamine:a-1,3-d-mannoside beta-1,4-n-acetylgluco
1373524_at	bcl2-associated transcription factor 1
1373536_at	,gb:aw525196 /db_xref=gi:7167581 /db_xref=ui-r-bj0p-aio-h-09-0-ui.s1 /clone=ui-r-bj0p-aio-h-09-0-ui /fea=est /cnt=10 /tid=rn.15245.1 /tier=stack /stk=8 /ug=rn.15245 /ug_title=ests
1373542_at	sphingosine kinase 2

Supplemental Data Table S4. Continued.

1373585_at	similar to riken cdna 1810020g14 (predicted)
1373590_at	stomatin
1373618_at	camp responsive element binding protein-like 2
1373625_at	serine hydroxymethyl transferase 1 (soluble)
1373639_at	similar to riken cdna 2410022l05
1373645_at	matrix metalloproteinase 1a (interstitial collagenase) (predicted)
1373667_at	cysteine conjugate-beta lyase
1373685_at	similar to low density lipoprotein receptor-related protein binding protein
1373693_at	g protein-coupled receptor, family c, group 5, member c
1373854_at	,gb:ai175795 /db_xref=gi:3726433 /db_xref=est219365 /clone=rovbf52 /fea=est /cnt=12 /tid=rn.3583.1 /tier=stack /stk=7 /ug=rn.3583 /ug_title=ests
1373859_at	,gb:aa819884 /db_xref=gi:4228136 /db_xref=ui-r-a0-aq-b-08-0-ui.s1 /clone=ui-r-a0-aq-b-08-0-ui /fea=est /cnt=12 /tid=rn.2285.1 /tier=stack /stk=7 /ug=rn.2285 /ug_title=ests
1373901_at	similar to s-cabp2 (predicted)
1373909_at	,gb:ai175507 /db_xref=gi:3726145 /db_xref=est219059 /clone=rmuco35 /fea=est /cnt=12 /tid=rn.3984.1 /tier=stack /stk=7 /ug=rn.3984 /ug_title=ests
1373921_at	fucosyltransferase 7
1373975_at	similar to thioether s-methyltransferase
1373978_at	nuclear cap binding protein subunit 1, 80kda
1373986_at	,gb:ai410107 /db_xref=gi:4253611 /db_xref=est238400 /clone=rkiea51 /fea=est /cnt=10 /tid=rn.20036.1 /tier=stack /stk=7 /ug=rn.20036 /ug_title=ests
1373990_at	similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 12
1373990_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 12
1374006_at	kynurenine aminotransferase iii
1374101_at	tbc1 domain family, member 10
1374142_at	similar to riken cdna e130201n16 (predicted)
1374200_at, 1374221_at	solute carrier family 29 (nucleoside transporters), member 3
1374213_at	adp-ribosylation factor guanine nucleotide-exchange factor 2 (brefeldin a-inhibited)
1374217_at	similar to chromosome 16 open reading frame 5
1374218_at	similar to kiaa0522 protein
1374222_at	tumor suppressing subtransferable candidate 5
1374239_at	ferm, rhogef and pleckstrin domain protein 2 (predicted)
1374241_at	,gb:ai406271 /db_xref=gi:4249775 /db_xref=est234557 /clone=rbrdl82 /fea=est /cnt=7 /tid=rn.23363.1 /tier=stack /stk=7 /ug=rn.23363 /ug_title=ests
1374244_at	ab2-060
1374254_a_at	hypothetical loc300441
1374272_at	,gb:bi280268 /db_xref=gi:14928881 /db_xref=ui-r-de0-cag-a-01-0-ui.s1 /clone=ui-r-de0-cag-a-01-0-ui /fea=est /cnt=7 /tid=rn.16280.1 /tier=stack /stk=7 /ug=rn.16280 /ug_title=ests
1374420_at	similar to riken cdna 2310001a20
1374440_at	dehydrogenase/reductase (sdr family) member 8
1374475_at	abhydrolase domain containing 1
1374478_at	similar to riken cdna 2610528j11 (predicted)
1374487_at	similar to riken cdna 5730536a07
1374512_at	cadherin 7, type 2

Supplemental Data Table S4. Continued.

1374522_at	leucine-rich repeat lgi family, member 3 (predicted)
1374524_at	selenocysteine lyase
1374527_at	similar to hypothetical protein d4ertd765e (predicted)
1374546_at	protocadherin 17 (predicted)
1374558_at	similar to b7-like protein gl50-b
1374610_at	similar to hypothetical protein 4933408f15
1374613_at	,gb:be100609 /db_xref=gi:8492505 /db_xref=ui-r-bj1-auk-d-06-0-ui.s1 /clone=ui-r-bj1-auk-d-06-0-ui /fea=est /cnt=9 /tid=rn.13909.1 /tier=stack /stk=6 /ug=rn.13909 /ug_title=ests
1374624_at	udp-n-acetyl-alpha-d-galactosamine:polypeptide n-acetylgalactosaminyltransferase 11 (galnac-t11)
1374625_at	hairy and enhancer of split 6 (drosophila)
1374628_at	crystallin, zeta
1374638_at	peroxisomal biogenesis factor 13 (predicted)
1374641_at	,gb:bf397653 /db_xref=gi:11382637 /db_xref=ui-r-bs2-bed-a-09-0-ui.s1 /clone=ui-r-bs2-bed-a-09-0-ui /fea=est /cnt=8 /tid=rn.40613.1 /tier=stack /stk=6 /ug=rn.40613 /ug_title=ests
1374657_at	similar to riken cdna 1810020d17
1374709_at	,gb:ai406795 /db_xref=gi:4250299 /db_xref=est235082 /clone=rbrdi44 /fea=est /cnt=9 /tid=rn.19878.1 /tier=stack /stk=6 /ug=rn.19878 /ug_title=ests
1374749_at	similar to riken cdna 2010015j01
1374758_at	,gb:bm387112 /db_xref=gi:18187165 /db_xref=ui-r-cn1-cji-o-12-0-ui.s1 /clone=ui-r-cn1-cji-o-12-0-ui /fea=est /cnt=7 /tid=rn.3315.1 /tier=stack /stk=6 /ug=rn.3315 /ug_title=ests
1374800_at	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15
1374833_at	,gb:bf290953 /db_xref=gi:11222023 /db_xref=est455544 /clone=rgiig77 /fea=est /cnt=7 /tid=rn.24673.1 /tier=stack /stk=6 /ug=rn.24673 /ug_title=ests
1374846_at	cardiac lineage protein 1
1374871_at, 1387966_at	asparaginase-like sperm autoantigen
1374892_at	spermidine/spermine n1-acetyl transferase 2 (predicted)
1374959_at	nad(p)h dehydrogenase, quinone 2
1374963_s_at	,gb:bi290604 /db_xref=gi:14949327 /db_xref=ui-r-dk0-cfx-b-11-0-ui.s1 /clone=ui-r-dk0-cfx-b-11-0-ui /fea=est /cnt=6 /tid=rn.15248.1 /tier=stack /stk=6 /ug=rn.15248 /ug_title=ests
1375026_at	ceroid-lipofuscinosis, neuronal 6 (predicted)
1375106_at, 1391409_at	amnionless (predicted)
1375120_at, 1375183_at	inhibitor of dna binding 4
1375146_at	similar to riken cdna 3010027g13
1375173_at	rdcr-0918-3 protein
1375197_at	,gb:bg665384 /db_xref=gi:13887306 /db_xref=draccb07 /clone=draccb07 /fea=est /cnt=25 /tid=rn.3254.1 /tier=stack /stk=15 /ug=rn.3254 /ug_title=ests, moderately similar to ucry_human ubiquinol-cytochrome c reductase complex 6.4 kd protein (h.sapiens)
1375247_at, 1388644_at	monoglyceride lipase
1375267_at	peptidylprolyl isomerase c
1375357_at	dystonia 1

Supplemental Data Table S4. Continued.

1375411_at	nadh dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (b14.5a) (predicted)
1375428_at, 1381968_at	cellular repressor of e1a-stimulated genes (predicted)
1375436_at	nicotinate phosphoribosyltransferase-like protein
1375516_at	nadh dehydrogenase (ubiquinone) 1, subcomplex unknown, 2
1375526_at	similar to novel protein of unknown function (duf423) family member
1375560_at, 1390421_at	similar to riken cdna 0610010d20 (predicted)
1375579_at	,gb:bg377374 /db_xref=gi:13301846 /db_xref=ui-r-cu0-bvc-g-02-0-ui.s1 /clone=ui-r-cu0-bvc-g-02-0-ui /fea=est /cnt=8 /tid=rn.41151.1 /tier=stack /stk=7 /ug=rn.41151 /ug_title=ests
1375785_at	similar to hypothetical protein d4ertd89e
1375856_at	,gb:ai102258 /db_xref=gi:3707059 /db_xref=est211547 /clone=rbrcb22 /fea=est /cnt=13 /tid=rn.7450.1 /tier=consend /stk=5 /ug=rn.7450 /ug_title=ests, moderately similar to bi54 mouse brain protein i54 (m.musculus)
1375934_at	similar to riken cdna d330045a20
1375944_at	acetyl-coenzyme a synthetase 2 (adp forming) (predicted)
1375997_at	,gb:aa799503 /db_xref=gi:2862458 /db_xref=est189000 /clone=rheab81 /fea=est /cnt=8 /tid=rn.3768.1 /tier=consend /stk=5 /ug=rn.3768 /ug_title=ests
1376007_at	similar to cgi-121 protein
1376051_at	crystallin, lamda 1
1376078_at	,gb:bi296274 /db_xref=gi:14960555 /db_xref=ui-r-dk0-cey-d-07-0-ui.s1 /clone=ui-r-dk0-cey-d-07-0-ui /fea=est /cnt=7 /tid=rn.22415.1 /tier=consend /stk=5 /ug=rn.22415 /ug_title=ests
1376107_at	arginase 2
1376117_at	ng22 protein
1376119_at	similar to thyroid adenoma associated
1376128_at	,gb:ai103937 /db_xref=gi:3704874 /db_xref=est213226 /clone=rhebv35 /fea=est /cnt=6 /tid=rn.17851.1 /tier=consend /stk=5 /ug=rn.17851 /ug_title=ests
1376163_at	similar to expressed sequence ai649392
1376187_at	,gb:ai177887 /db_xref=gi:3728525 /db_xref=est221537 /clone=rplch94 /fea=est /cnt=6 /tid=rn.19332.1 /tier=consend /stk=5 /ug=rn.19332 /ug_title=ests
1376209_at	similar to hypothetical protein supported by al449243 (predicted)
1376248_at	sulfotransferase family, cytosolic, 2b, member 1 (predicted)
1376431_at	endoplasmic reticulum chaperone sil1 homolog (s. cerevisiae)
1376595_at	similar to peroxisome biogenesis factor 1
1376605_at	solute carrier family 17 (anion/sugar transporter), member 5
1376656_at	ubiquitin specific protease 20 (predicted)
1376702_at	megalencephalic leukoencephalopathy with subcortical cysts 1 (predicted)
1376709_at	solute carrier family 39 (metal ion transporter), member 8
1376723_a_at	,gb:aw142765 /db_xref=gi:6162664 /db_xref=est293018 /clone=rgiav08 /fea=est /cnt=7 /tid=rn.40208.1 /tier=consend /stk=4 /ug=rn.40208 /ug_title=ests
1376728_at	protein phosphatase 1, regulatory (inhibitor) subunit 8 (predicted)
1376746_at, 1382061_at	lactate dehydrogenase d
1376765_at	similar to maestro

Supplemental Data Table S4. Continued.

1376785_at	synaptonemal complex protein 3
1376808_at	,gb:bg672572 /db_xref=gi:13894671 /db_xref=drncle11 /clone=drncle11 /fea=est /cnt=6 /tid=rn.21871.1 /tier=consend /stk=4 /ug=rn.21871 /ug_title=ests
1376852_at	methylcrotonoyl-coenzyme a carboxylase 1 (alpha)
1376868_at	cobl-like 1 (predicted)
1376885_at	similar to chemokine-like factor super family 4
1377019_at	,gb:bf410042 /db_xref=gi:11398017 /db_xref=ui-r-ca0-bjs-h-01-0-ui.s1 /clone=ui-r-ca0-bjs-h-01-0-ui /fea=est /cnt=5 /tid=rn.31227.1 /tier=consend /stk=4 /ug=rn.31227 /ug_title=ests
1377029_at	rar-related orphan receptor alpha (predicted)
1377033_at	serine (or cysteine) proteinase inhibitor, clade f, member 2
1377048_at	similar to cdna sequence bc021917
1377051_at	mpv17 transgene, kidney disease mutant-like (predicted)
1377060_at	methylcrotonoyl-coenzyme a carboxylase 2 (beta)
1377085_at	carbonic anhydrase 7 (predicted)
1377088_at	similar to riken cdna 2310046k01
1377135_at	,gb:aa944958 /db_xref=gi:3104874 /db_xref=est200457 /clone=rkiau88 /fea=est /cnt=5 /tid=rn.22711.1 /tier=consend /stk=4 /ug=rn.22711 /ug_title=ests
1377232_at	similar to hypothetical protein (predicted)
1377266_at	,gb:ai071674 /db_xref=gi:3397889 /db_xref=ui-r-c1-ku-e-12-0-ui.s2 /clone=ui-r-c1-ku-e-12-0-ui /fea=est /cnt=4 /tid=rn.20599.1 /tier=consend /stk=4 /ug=rn.20599 /ug_title=ests
1377333_at	,gb:be114427 /db_xref=gi:8506532 /db_xref=ui-r-ca0-axm-b-04-0-ui.s1 /clone=ui-r-ca0-axm-b-04-0-ui /fea=est /cnt=4 /tid=rn.18255.1 /tier=consend /stk=4 /ug=rn.18255 /ug_title=ests
1377351_at	sushi domain containing 3 (predicted)
1377375_at	aminoadipate-semialdehyde synthase (predicted)
1377576_at	similar to riken cdna 1110013g13 (predicted)
1377719_a_at	,gb:aa892765 /db_xref=gi:3019644 /db_xref=est196568 /clone=rkiax04 /fea=est /cnt=7 /tid=rn.3800.2 /tier=consend /stk=3 /ug=rn.3800 /ug_title=ests
1377821_at	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)
1378307_at	pleckstrin homology domain containing, family h (with myth4 domain) member 1 (predicted)
1378536_at	,gb:ai638960 /db_xref=gi:4699994 /db_xref=rx00909s /clone=rx00909 /fea=est /cnt=3 /tid=rn.16596.1 /tier=consend /stk=3 /ug=rn.16596 /ug_title=ests
1379044_at	similar to riken cdna 1700108l22
1379243_at	nadh dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (b14) (predicted)
1379250_at, 1385072_at	galactose mutarotase
1379371_at	,gb:bf284791 /db_xref=gi:11215861 /db_xref=est449382 /clone=rgiew38 /fea=est /cnt=7 /tid=rn.25117.1 /tier=consend /stk=2 /ug=rn.25117 /ug_title=ests
1379703_at	hypothetical loc315055 (predicted)
1380546_at	similar to hypothetical protein flj10986
1380546_at	similar to hypothetical protein flj10986
1380600_at	similar to glycoprotein iib - rat
1380905_at	,gb:aa893260 /db_xref=gi:4132271 /db_xref=est197063 /clone=rkibe21 /fea=est /cnt=2 /tid=rn.40554.1 /tier=consend /stk=2 /ug=rn.40554 /ug_title=ests

Supplemental Data Table S4. Continued.

1381951_at	,gb:bf408414 /db_xref=gi:11396389 /db_xref=ui-r-bj2-brc-e-02-0-ui.s1 /clone=ui-r-bj2-brc-e-02-0-ui /fea=est /cnt=2 /tid=rn.14722.1 /tier=consend /stk=2 /ug=rn.14722 /ug_title=ests
1382683_a_at	,gb:aa891943 /db_xref=gi:3018822 /db_xref=est195746 /clone=rkiai86 /fea=est /cnt=1 /tid=rn.3564.2 /tier=consend /stk=1 /ug=rn.3564 /ug_title=ests
1382997_at	solute carrier family 22 (organic cation transporter), member 13 (predicted)
1383058_at	,gb:ai410438 /db_xref=gi:4253942 /db_xref=est238731 /clone=rhecs72 /fea=est /cnt=21 /tid=rn.4287.1 /tier=consend /stk=0 /ug=rn.4287 /ug_title=ests
1383061_at	,gb:ai070680 /db_xref=gi:3396931 /db_xref=ui-r-c2-mx-d-05-0-ui.s1 /clone=ui-r-c2-mx-d-05-0-ui /fea=est /cnt=24 /tid=rn.14666.1 /tier=consend /stk=0 /ug=rn.14666 /ug_title=ests
1383161_a_at	,gb:ai008646 /db_xref=gi:4132919 /db_xref=est203097 /clone=rembb18 /fea=est /cnt=8 /tid=rn.3800.3 /tier=consend /stk=0 /ug=rn.3800 /ug_title=ests
1383165_at	similar to kiaa1324 protein (predicted)
1384008_at	similar to hypothetical protein flj40283 (predicted)
1384027_a_at	,gb:ai072042 /db_xref=gi:3398236 /db_xref=ui-r-c2-nd-g-08-0-ui.s1 /clone=ui-r-c2-nd-g-08-0-ui /fea=est /cnt=4 /tid=rn.20680.1 /tier=consend /stk=0 /ug=rn.20680 /ug_title=ests
1384028_at	,gb:ai072042 /db_xref=gi:3398236 /db_xref=ui-r-c2-nd-g-08-0-ui.s1 /clone=ui-r-c2-nd-g-08-0-ui /fea=est /cnt=4 /tid=rn.20680.1 /tier=consend /stk=0 /ug=rn.20680 /ug_title=ests
1384164_at	,gb:bf290416 /db_xref=gi:11221486 /db_xref=est455007 /clone=rgihv60 /fea=est /cnt=3 /tid=rn.6639.1 /tier=consend /stk=0 /ug=rn.6639 /ug_title=ests
1384474_at	,gb:aa860010 /db_xref=gi:4230542 /db_xref=ui-r-e0-ca-c-07-0-ui.s1 /clone=ui-r-e0-ca-c-07-0-ui /fea=est /cnt=2 /tid=rn.872.1 /tier=consend /stk=0 /ug=rn.872 /ug_title=ests
1385035_at	ubiquitin specific protease 12 (predicted)
1385088_at	hypothetical loc304650 (predicted)
1386045_at	similar to krab zinc finger protein kr18
1386280_at	similar to riken cdna 0610006f02
1386454_at	solute carrier family 23 (nucleobase transporters), member 3 (predicted)
1386867_at	brain protein 44-like
1386870_at	glutamate-ammonia ligase (glutamine synthase)
1386871_at	glutathione peroxidase 4
1386885_at	enoyl coenzyme a hydratase 1, peroxisomal
1386886_at	cd164 antigen
1386887_at	cytochrome c oxidase subunit vb
1386891_at	phosphatidylethanolamine binding protein
1386898_at	heat shock 10 kda protein 1
1386904_a_at	cytochrome b-5
1386916_at	aconitase 1
1386917_at	pyruvate carboxylase
1386938_at	alanyl (membrane) aminopeptidase
1386943_at	transmembrane 4 superfamily member 11
1386953_at	hydroxysteroid 11-beta dehydrogenase 1
1386954_at	adenylate kinase 2
1386960_at	solute carrier family 37 (glycerol-6-phosphate transporter), member 4
1386980_at	apolipoprotein m
1387010_s_at	sodium channel, voltage-gated, type i, beta polypeptide
1387013_at	kidney-specific membrane protein

Supplemental Data Table S4. Continued.

1387053_at	flavin containing monooxygenase 1
1387058_at	phosphatidylcholine transfer protein
1387139_at	hydroxyacid oxidase 2 (long chain)
1387158_at	meprin 1 beta
1387178_a_at	cystathionine beta synthase
1387218_at	trefoil factor 3
1387223_at	aminoadipate aminotransferase
1387232_at	bone morphogenetic protein 4
1387234_at	alpha-2-glycoprotein 1, zinc
1387244_at	cell growth regulator with ring finger domain 1
1387253_at	guanylate cyclase activator 2b
1387284_at	dihydropyrimidinase
1387296_at	cytochrome p450, family 2, subfamily j, polypeptide 4
1387303_at	solute carrier family 22 (organic cation transporter), member 2
1387314_at	sulfotransferase family 1b, member 1
1387336_at	n-acetyltransferase 8 (camello like)
1387344_at	aldehyde dehydrogenase family 6, subfamily a1
1387357_at	trimethyllysine hydroxylase, epsilon
1387365_at	nuclear receptor subfamily 1, group h, member 3
1387372_at	solute carrier family 6 (neurotransmitter transporter, gaba), member 13
1387375_at	ketohexokinase
1387382_at	histamine n-methyltransferase
1387531_at	methionine sulfoxide reductase a
1387567_at	hypothetical gene supported by nm_017111
1387567_at	solute carrier family (organic anion transporter) member 3
1387669_a_at	epoxide hydrolase 1, microsomal
1387672_at	glycine n-methyltransferase
1387737_at	methionine adenosyltransferase ii, alpha
1387791_at	angiotensin 1 converting enzyme
1387793_at	erm-binding phosphoprotein
1387799_at	fxyd domain-containing ion transport regulator 2
1387805_at	bcl2/adenovirus e1b 19 kda-interacting protein 3
1387811_at	angiotensinogen
1387819_at	elastase 1, pancreatic
1387859_at	nitrogen fixation gene 1 (s. cerevisiae)
1387867_at	aldehyde dehydrogenase family 9, subfamily a1
1387877_at	formiminotransferase cyclodeaminase
1387889_at	folate receptor 1 (adult)
1387959_at	lysophospholipase
1387972_at	mucin and cadherin like
1387987_at	solute carrier family 22 (organic anion transporter), member 19
1388097_at	calcium channel, voltage-dependent, gamma subunit 5
1388113_at	cytochrome c oxidase, subunit viiia
1388118_at	3-hydroxyisobutyrate dehydrogenase
1388145_at	tenascin xa
1388160_a_at	isocitrate dehydrogenase 3 (nad+) beta
1388163_at	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
1388167_at	nuclear factor i/b

Supplemental Data Table S4. Continued.

1388172_at	solute carrier family 22 (organic anion/cation transporter), member 9
1388176_at	camello-like 5
1388199_at	tumor-associated calcium signal transducer 1
1388300_at	microsomal glutathione s-transferase 3 (predicted)
1388301_at	ubiquinol-cytochrome c reductase core protein i
1388315_at	similar to neuronal protein 15.6
1388323_at	nadh dehydrogenase (ubiquinone) 1 alpha subcomplex, 9
1388324_at	nitrilase 1
1388326_at	nadh dehydrogenase (ubiquinone) fe-s protein 8 (predicted)
1388327_at	similar to dna segment, chr 10, erato doi 214, expressed (predicted)
1388330_at	vitamin k epoxide reductase complex, subunit 1
1388343_at	nadh dehydrogenase (ubiquinone) 1 beta subcomplex, 7 (predicted)
1388358_at	electron-transfer-flavoprotein, beta polypeptide
1388361_at	nadh dehydrogenase (ubiquinone) 1 beta subcomplex, 10 (predicted)
1388364_at	nadh dehydrogenase (ubiquinone) fe-s protein 3 (predicted)
1388365_at	atpase, h+ transporting, v0 subunit d isoform 1
1388374_at	,gb:ai412011 /db_xref=gi:4255515 /db_xref=est240305 /clone=rkiej50 /fea=est /cnt=27 /tid=rn.3738.1 /tier=stack /stk=21 /ug=rn.3738 /ug_title=ests
1388380_at	similar to protein cgi-51
1388391_at	similar to nadh dehydrogenase
1388441_at	,gb:bg379987 /db_xref=gi:13304459 /db_xref=ui-r-cs0-bto-f-05-0-ui.s1 /clone=ui-r-cs0-bto-f-05-0-ui /fea=est /cnt=35 /tid=rn.64564.1 /tier=stack /stk=17 /ug=rn.64564 /ug_title=ests
1388463_at	testis expressed gene 264 homolog (mouse)
1388489_at	nadh dehydrogenase (ubiquinone) 1 alpha subcomplex, 3 (predicted)
1388491_at	ring finger protein 153 (predicted)
1388526_at	,gb:ai169075 /db_xref=gi:3705383 /db_xref=est214904 /clone=rkibm70 /fea=est /cnt=18 /tid=rn.3691.1 /tier=stack /stk=15 /ug=rn.3691 /ug_title=ests, weakly similar to gto1_rat glutathione transferase omega 1 (gsto 1-1) (glutathione-dependent dehydroascorbate reductase) (r.norvegicus)
1388537_at, 1390454_at	4-nitrophenylphosphatase domain and non-neuronal snap25-like protein homolog 1 (c. elegans)
1388546_at	,gb:ai013328 /db_xref=gi:3227384 /db_xref=est208003 /clone=rspbj58 /fea=est /cnt=15 /tid=rn.7574.1 /tier=stack /stk=15 /ug=rn.7574 /ug_title=ests
1388558_at	adenylate kinase 3
1388569_at	serine (or cysteine) proteinase inhibitor, clade f), member 1
1388570_at	similar to riken cdna 2310005o14
1388579_at	similar to hypothetical gene mgc19595 (predicted)
1388611_at	transcription elongation factor a (sii), 3
1388617_at	biphenyl hydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen)
1388626_at	similar to chromosome 20 open reading frame 116 (predicted)
1388634_at	phosphoglucomutase 1
1388738_at	similar to mkiaa0534 protein
1388751_at	rna binding motif protein 24 (predicted)
1388778_at	,gb:bf284876 /db_xref=gi:11215946 /db_xref=est449467 /clone=rgiex35 /fea=est /cnt=15 /tid=rn.17629.1 /tier=stack /stk=11 /ug=rn.17629 /ug_title=ests
1388788_at	glutaryl-coenzyme a dehydrogenase (predicted)
1388814_at	dead (asp-glu-ala-asp) box polypeptide 19

Supplemental Data Table S4. Continued.

1388883_at	polymerase (dna-directed), delta 4
1388919_at	zinc finger protein 541 (predicted)
1388926_at	ectonucleotide pyrophosphatase/phosphodiesterase 5
1388948_at	start domain containing 10
1388980_at	unknown (protein for mgc:72560)
1388988_at	similar to riken cdna 1810013b01
1388998_at	erythrocyte protein band 4.9 (predicted)
1389012_at	nadh dehydrogenase (ubiquinone) 1 beta subcomplex, 2 (predicted)
1389032_at	mucolipin 1 (predicted)
1389066_at	down syndrome critical region gene 1-like 1
1389113_at	similar to hypothetical protein mgc32471 (predicted)
1389114_at	similar to hypothetical protein mgc59076
1389154_at	lipoic acid synthetase
1389166_at	calcium and integrin binding family member 2
1389229_at	similar to riken cdna c130099a20
1389234_at	von willebrand factor
1389251_at	nudix (nucleoside diphosphate linked moiety x)-type motif 7 (predicted)
1389288_at	nadh dehydrogenase (ubiquinone) 1 alpha subcomplex, 2 (predicted)
1389307_at	similar to amyloid beta (a4) precursor-like protein 1
1389350_at	apolipoprotein h
1389354_at	similar to semaf cytoplasmic domain associated protein 2
1389465_at	,gb:ai231286 /db_xref=gi:3815166 /db_xref=est227974 /clone=remdi17 /fea=est /cnt=8 /tid=rn.20167.1 /tier=stack /stk=7 /ug=rn.20167 /ug_title=ests
1389469_at	chromodomain helicase dna binding protein 1-like (predicted)
1389548_at	alcohol dehydrogenase, iron containing, 1
1389549_at	proline synthetase co-transcribed (predicted)
1389632_at	rho-related btb domain containing 1 (predicted)
1389678_at	,gb:bm389496 /db_xref=gi:18189549 /db_xref=ui-r-cn1-cjn-n-03-0-ui.s1 /clone=ui-r-cn1-cjn-n-03-0-ui /fea=est /cnt=7 /tid=rn.38259.1 /tier=stack /stk=6 /ug=rn.38259 /ug_title=ests
1389695_at	family with sequence similarity 20, member c (predicted)
1389704_at	,gb:aa850490 /db_xref=gi:2938030 /db_xref=est193257 /clone=rovag33 /fea=est /cnt=7 /tid=rn.7010.1 /tier=stack /stk=6 /ug=rn.7010 /ug_title=ests
1389716_at	loc501614
1389725_at	transmembrane 7 superfamily member 2
1389744_at	loc499898
1389757_at	similar to acetyl-coa dehydrogenase -related (111.6 kd) (5g231) (predicted)
1389785_at	similar to riken cdna 0610006h10 gene
1389786_at	similar to riken cdna 2410005o16
1389820_at	endonuclease/reverse transcriptase
1389845_at	dnaj (hsp40) homolog, subfamily a, member 3 (predicted)
1389866_at	loc499187
1389907_at	similar to archease
1389963_at	dead/h (asp-glu-ala-asp/his) box polypeptide 26
1390021_at	histone 1, h2bh
1390126_at	,gb:be112913 /db_xref=gi:8505018 /db_xref=ui-r-bj1-awa-c-09-0-ui.s1 /clone=ui-r-bj1-awa-c-09-0-ui /fea=est /cnt=9 /tid=rn.12932.1 /tier=consend /stk=5 /ug=rn.12932 /ug_title=ests

Supplemental Data Table S4. Continued.

1390164_at	,gb:be099850 /db_xref=gi:8491732 /db_xref=ui-r-bj1-atq-h-09-0-ui.s1 /clone=ui-r-bj1-atq-h-09-0-ui /fea=est /cnt=7 /tid=rn.23225.1 /tier=consend /stk=5 /ug=rn.23225 /ug_title=ests
1390172_at	dehydrogenase e1 and transketolase domain containing 1
1390219_at	similar to wd repeat membrane protein (predicted)
1390228_at	,gb:bm384446 /db_xref=gi:18184499 /db_xref=ui-r-cn1-cjn-m-12-0-ui.s1 /clone=ui-r-cn1-cjn-m-12-0-ui /fea=est /cnt=6 /tid=rn.31695.1 /tier=consend /stk=5 /ug=rn.31695 /ug_title=ests
1390285_at	similar to bc026645 protein
1390292_at	transmembrane protein 8 (five membrane-spanning domains) (predicted)
1390366_at	similar to pc-lkc gene product
1390406_at	rho gtpase activating protein 18 (predicted)
1390416_at	solute carrier family 25, member 30
1390498_at	,gb:ai230554 /db_xref=gi:3814426 /db_xref=est227234 /clone=remcx79 /fea=est /cnt=6 /tid=rn.23623.1 /tier=consend /stk=4 /ug=rn.23623 /ug_title=ests
1390508_at	similar to hypothetical protein mgc27648 (predicted)
1390569_at	similar to carnosinase 1
1390591_at	na/pi cotransporter 4
1390592_at	,gb:bm389412 /db_xref=gi:18189465 /db_xref=ui-r-cn1-cjk-m-05-0-ui.s1 /clone=ui-r-cn1-cjk-m-05-0-ui /fea=est /cnt=5 /tid=rn.43752.1 /tier=consend /stk=4 /ug=rn.43752 /ug_title=ests, moderately similar to t14273 zinc finger protein 106 - mouse (m.musculus)
1390598_at	,gb:bi294871 /db_xref=gi:14957748 /db_xref=ui-r-dk0-ced-b-03-0-ui.s1 /clone=ui-r-dk0-ced-b-03-0-ui /fea=est /cnt=5 /tid=rn.32717.1 /tier=consend /stk=4 /ug=rn.32717 /ug_title=ests
1390656_at	,gb:bf389473 /db_xref=gi:11374306 /db_xref=ui-r-cj0-bfc-b-11-0-ui.s1 /clone=ui-r-cj0-bfc-b-11-0-ui /fea=est /cnt=4 /tid=rn.64376.1 /tier=consend /stk=4 /ug=rn.64376 /ug_title=ests
1390807_at	carbonic anhydrase vb, mitochondrial
1391273_at	na+ dependent glucose transporter 1
1391485_at	,gb:bf290955 /db_xref=gi:11222025 /db_xref=est455546 /clone=rgiig78 /fea=est /cnt=6 /tid=rn.43745.1 /tier=consend /stk=2 /ug=rn.43745 /ug_title=ests
1391544_at	similar to adiponutrin
1392484_at	hypothetical loc299262
1392530_at	similar to nadh dehydrogenase (ubiquinone) 1, subcomplex unknown, 1
1392713_a_at	,gb:aa892541 /db_xref=gi:3019420 /db_xref=est196344 /clone=rkias65 /fea=est /cnt=3 /tid=rn.22980.1 /tier=consend /stk=1 /ug=rn.22980 /ug_title=ests
1393061_at	similar to cdna sequence bc021608
1393221_at	similar to 20-alpha-hydroxysteroid dehydrogenase
1394228_at	,gb:aa893147 /db_xref=gi:3020026 /db_xref=est196950 /clone=rkibc70 /fea=est /cnt=1 /tid=rn.13478.1 /tier=consend /stk=1 /ug=rn.13478 /ug_title=est
1398253_at	kidney androgen regulated protein
1398255_at	solute carrier family 15 (h+/peptide transporter), member 2
1398267_at	solute carrier family 22 (organic anion transporter), member 7
1398282_at	kynureninase (l-kynurenine hydrolase)
1398286_at	cysteine sulfinic acid decarboxylase
1398296_at	membrane interacting protein of rgs16
1398317_at	bisphosphate 3'-nucleotidase 1

Supplemental Data Table S4. Continued.

1398326_at	similar to nur77 downstream protein 2
1398341_at	hypothetical loc287661
1398350_at	brain abundant, membrane attached signal protein 1
1398360_at	hypothetical protein
1398378_at	glutathione s-transferase kappa 1
1398430_at	,gb:aw524711 /db_xref=gi:7167096 /db_xref=ui-r-bo0-aib-e-04-0-ui.s1 /clone=ui-r-bo0-aib-e-04-0-ui /fea=est /cnt=9 /tid=rn.8814.1 /tier=consend /stk=5 /ug=rn.8814 /ug_title=ests
1398612_at	aldo-keto reductase family 1, member c12 (predicted)
1398763_at	similar to translocase of inner mitochondrial membrane 23 homolog
1398763_at	translocase of inner mitochondrial membrane 23 homolog (yeast)
1398790_at	protein phosphatase 2a, catalytic subunit, alpha isoform
1398807_at	protein phosphatase 1b, magnesium dependent, beta isoform
1398839_at	thioredoxin 1
1398891_at	mitochondrial ribosomal protein l15 (predicted)
1398932_at	histidine triad nucleotide binding protein 1 (predicted)
1398962_at	uncharacterized protein family upf0227 member rgd1359682
1398991_at	phosphoprotein enriched in astrocytes 15
1399052_at	toll interacting protein (predicted)
1399065_at	similar to ai449441 protein (predicted)
1399068_at	similar to riken cdna 9430098e02
1399082_at	,gb:ai176581 /db_xref=gi:3727219 /db_xref=est220169 /clone=rovbu14 /fea=est /cnt=13 /tid=rn.12122.1 /tier=stack /stk=6 /ug=rn.12122 /ug_title=ests
1399109_at	,gb:bi281673 /db_xref=gi:14931647 /db_xref=ui-r-ct0s-cav-b-07-0-ui.s1 /clone=ui-r-ct0s-cav-b-07-0-ui /fea=est /cnt=6 /tid=rn.7769.1 /tier=consend /stk=4 /ug=rn.7769 /ug_title=ests

Supplemental Data Table S5. Biological Processes/Pathways with Over-representation of Genes among the Differentially Expressed Genes Following D-Serine Treatment as Determined by Searchong the NIAID DAVID databases.

Database	Term	Cl
GOTERM_BP_ALL	actin cytoskeleton organization and biogenesis	
GOTERM_BP_ALL	actin filament depolymerization	
GOTERM_BP_ALL	actin filament organization	
GOTERM_BP_ALL	actin filament polymerization	
GOTERM_BP_ALL	actin filament-based process	
KEGG_PATHWAY	ADHERENS JUNCTION	
GOTERM_BP_ALL	apoptosis	
GOTERM_BP_ALL	apoptotic program	
KEGG_PATHWAY	AXON GUIDANCE	
KEGG_PATHWAY	B CELL RECEPTOR SIGNALING PATHWAY	
GOTERM_BP_ALL	base-excision repair	
GOTERM_BP_ALL	biopolymer metabolism	
GOTERM_BP_ALL	caspase activation	
INTERPRO_NAME	Caspase Recruitment	
KEGG_PATHWAY	CELL COMMUNICATION	
GOTERM_BP_ALL	cell cycle	
GOTERM_BP_ALL	cell death	
GOTERM_BP_ALL	cell differentiation	
GOTERM_BP_ALL	cell division	
GOTERM_BP_ALL	cell motility	
GOTERM_BP_ALL	cell organization and biogenesis	
GOTERM_BP_ALL	cell projection biogenesis	
GOTERM_BP_ALL	cell projection organization and biogenesis	
GOTERM_BP_ALL	cell proliferation	
GOTERM_BP_ALL	cellular biosynthesis	
GOTERM_BP_ALL	cellular localization	
GOTERM_BP_ALL	cellular macromolecule metabolism	
GOTERM_BP_ALL	cellular morphogenesis	
GOTERM_BP_ALL	cellular protein metabolism	
GOTERM_BP_ALL	chromatin assembly	
GOTERM_BP_ALL	chromosome organization and biogenesis	
GOTERM_BP_ALL	cytokinesis	
GOTERM_BP_ALL	cytoplasm organization and biogenesis	
GOTERM_BP_ALL	cytoskeleton organization and biogenesis	
GOTERM_BP_ALL	cytoskeleton-dependent intracellular transport	
GOTERM_BP_ALL	death	
SP_PIR_KEYWORDS	DNA damage	
GOTERM_BP_ALL	DNA metabolism	
GOTERM_BP_ALL	DNA packaging	
GOTERM_BP_ALL	DNA repair	
GOTERM_BP_ALL	DNA replication	
GOTERM_BP_ALL	DNA-dependent DNA replication	
KEGG_PATHWAY	ECM-RECEPTOR INTERACTION	
GOTERM_BP_ALL	establishment and/or maintenance of chromatin architecture	

Supplemental Data Table S5. Continued.

GOTERM_BP_ALL	establishment of cellular localization	
GOTERM_BP_ALL	establishment of protein localization	
GOTERM_BP_ALL	establishment of RNA localization	
KEGG_PATHWAY	FOCAL ADHESION	
GOTERM_BP_ALL	I-kappaB kinase/NF-kappaB cascade	
GOTERM_BP_ALL	intercellular junction assembly and maintenance	
SP_PIR_KEYWORDS	interferon induction	
GOTERM_BP_ALL	intracellular protein transport	
GOTERM_BP_ALL	intracellular transport	
GOTERM_BP_ALL	lamellipodium biogenesis	
GOTERM_BP_ALL	localization of cell	
GOTERM_BP_ALL	locomotion	
GOTERM_BP_ALL	M phase of meiotic cell cycle	
GOTERM_BP_ALL	M phase of mitotic cell cycle	
GOTERM_BP_ALL	macromolecule biosynthesis	
GOTERM_BP_ALL	macromolecule metabolism	
GOTERM_BP_ALL	meiosis	
GOTERM_BP_ALL	meiotic cell cycle	
GOTERM_BP_ALL	microtubule cytoskeleton organization and biogenesis	
GOTERM_BP_ALL	microtubule-based movement	
GOTERM_BP_ALL	microtubule-based process	
GOTERM_BP_ALL	mitosis	
GOTERM_BP_ALL	mitotic cell cycle	
GOTERM_BP_ALL	morphogenesis of epithelia	
GOTERM_BP_ALL	mRNA metabolism	
GOTERM_BP_ALL	mRNA processing	
SP_PIR_KEYWORDS	mRNA splicing	
GOTERM_BP_ALL	mRNA transport	
GOTERM_BP_ALL	negative regulation of apoptosis	
GOTERM_BP_ALL	negative regulation of cell organization and biogenesis	
GOTERM_BP_ALL	negative regulation of cell proliferation	
GOTERM_BP_ALL	negative regulation of programmed cell death	
GOTERM_BP_ALL	negative regulation of protein metabolism	
GOTERM_BP_ALL	nuclear export	
GOTERM_BP_ALL	nuclear import	
GOTERM_BP_ALL	nuclear mRNA splicing, via spliceosome	
GOTERM_BP_ALL	nuclear transport	
GOTERM_BP_ALL	nucleic acid transport	
GOTERM_BP_ALL	nucleobase, nucleoside, nucleotide and nucleic acid metabolism	
GOTERM_BP_ALL	nucleobase, nucleoside, nucleotide and nucleic acid transport	
GOTERM_BP_ALL	nucleocytoplasmic transport	
GOTERM_BP_ALL	nucleosome assembly	
GOTERM_BP_ALL	oligosaccharide metabolism	
GOTERM_BP_ALL	organelle organization and biogenesis	
GOTERM_BP_ALL	positive regulation of caspase activity	
GOTERM_BP_ALL	positive regulation of epithelial cell proliferation	
GOTERM_BP_ALL	positive regulation of hydrolase activity	
GOTERM_BP_ALL	positive regulation of I-kappaB kinase/NF-kappaB cascade	

Supplemental Data Table S5. Continued.

GOTERM_BP_ALL	positive regulation of signal transduction	
GOTERM_BP_ALL	programmed cell death	
GOTERM_BP_ALL	protein biosynthesis	
GOTERM_BP_ALL	protein complex assembly	
GOTERM_BP_ALL	protein depolymerization	
GOTERM_BP_ALL	protein import	
GOTERM_BP_ALL	protein import into nucleus	
GOTERM_BP_ALL	protein localization	
GOTERM_BP_ALL	protein metabolism	
GOTERM_BP_ALL	protein polymerization	
GOTERM_BP_ALL	protein targeting	
GOTERM_BP_ALL	protein transport	
GOTERM_BP_ALL	Ras protein signal transduction	
KEGG_PATHWAY	REGULATION OF ACTIN CYTOSKELETON	
GOTERM_BP_ALL	regulation of actin filament length	
GOTERM_BP_ALL	regulation of actin filament polymerization	
GOTERM_BP_ALL	regulation of actin polymerization and/or depolymerization	
GOTERM_BP_ALL	regulation of apoptosis	
GOTERM_BP_ALL	regulation of caspase activity	
GOTERM_BP_ALL	regulation of cell cycle	
GOTERM_BP_ALL	regulation of cell migration	
GOTERM_BP_ALL	regulation of cell motility	
GOTERM_BP_ALL	regulation of cell organization and biogenesis	
GOTERM_BP_ALL	regulation of cell proliferation	
GOTERM_BP_ALL	regulation of cyclin dependent protein kinase activity	
GOTERM_BP_ALL	regulation of DNA metabolism	
GOTERM_BP_ALL	regulation of hydrolase activity	
GOTERM_BP_ALL	regulation of I-kappaB kinase/NF-kappaB cascade	
GOTERM_BP_ALL	regulation of programmed cell death	
GOTERM_BP_ALL	regulation of progression through cell cycle	
GOTERM_BP_ALL	regulation of protein metabolism	
GOTERM_BP_ALL	regulation of translational initiation	
GOTERM_BP_ALL	response to DNA damage stimulus	
KEGG_PATHWAY	RIBOSOME	
GOTERM_BP_ALL	RNA export from nucleus	
GOTERM_BP_ALL	RNA localization	
GOTERM_BP_ALL	RNA metabolism	
GOTERM_BP_ALL	RNA processing	
GOTERM_BP_ALL	RNA splicing	
GOTERM_BP_ALL	RNA splicing, via transesterification reactions	
GOTERM_BP_ALL	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	
GOTERM_BP_ALL	RNA transport	
GOTERM_BP_ALL	skeletal development	
GOTERM_BP_ALL	spindle organization and biogenesis	
KEGG_PATHWAY	TIGHT JUNCTION	
GOTERM_BP_ALL	transcription from RNA polymerase I promoter	
GOTERM_BP_ALL	translational initiation	
GOTERM_BP_ALL	transmembrane receptor protein tyrosine phosphatase signaling pathway	

Supplemental Data Table S5. Continued.

GOTERM_BP_ALL	organic acid metabolism	
GOTERM_BP_ALL	acetyl-CoA catabolism	
GOTERM_BP_ALL	acyl-CoA metabolism	
GOTERM_BP_ALL	aerobic respiration	
KEGG_PATHWAY	ALANINE AND ASPARTATE METABOLISM	
GOTERM_BP_ALL	alcohol metabolism	
GOTERM_BP_ALL	aldehyde metabolism	
GOTERM_BP_ALL	amine biosynthesis	
GOTERM_BP_ALL	amine catabolism	
GOTERM_BP_ALL	amino acid and derivative metabolism	
GOTERM_BP_ALL	amino acid biosynthesis	
GOTERM_BP_ALL	amino acid catabolism	
GOTERM_BP_ALL	amino acid derivative metabolism	
COG_KOG_ONTOLOGY	Amino acid transport and metabolism	
KEGG_PATHWAY	ARACHIDONIC ACID METABOLISM	
KEGG_PATHWAY	ARGININE AND PROLINE METABOLISM	
GOTERM_BP_ALL	aromatic compound biosynthesis	
GOTERM_BP_ALL	aromatic compound catabolism	
SP_PIR_KEYWORDS	aromatic hydrocarbons catabolism	
GOTERM_BP_ALL	aspartate family amino acid metabolism	
GOTERM_BP_ALL	ATP biosynthesis	
GOTERM_BP_ALL	ATP metabolism	
GOTERM_BP_ALL	ATP synthesis coupled electron transport	
GOTERM_BP_ALL	ATP synthesis coupled proton transport	
KEGG_PATHWAY	BETA-ALANINE METABOLISM	
GOTERM_BP_ALL	branched chain family amino acid metabolism	
KEGG_PATHWAY	BUTANOATE METABOLISM	
KEGG_PATHWAY	CAPROLACTAM DEGRADATION	
GOTERM_BP_ALL	carbohydrate metabolism	
KEGG_PATHWAY	CARBON FIXATION	
GOTERM_BP_ALL	carboxylic acid metabolism	
GOTERM_BP_ALL	cellular carbohydrate metabolism	
GOTERM_BP_ALL	cellular lipid metabolism	
GOTERM_BP_ALL	cellular respiration	
KEGG_PATHWAY	CITRATE CYCLE (TCA CYCLE)	
GOTERM_BP_ALL	coenzyme biosynthesis	
GOTERM_BP_ALL	coenzyme catabolism	
GOTERM_BP_ALL	cofactor biosynthesis	
GOTERM_BP_ALL	cofactor catabolism	
GOTERM_BP_ALL	cysteine metabolism	
SP_PIR_KEYWORDS	detoxification	
GOTERM_BP_ALL	electron transport	
GOTERM_BP_ALL	fatty acid beta-oxidation	
GOTERM_BP_ALL	fatty acid metabolism	
GOTERM_BP_ALL	fatty acid oxidation	
GOTERM_BP_ALL	folic acid and derivative metabolism	
GOTERM_BP_ALL	generation of precursor metabolites and energy	
GOTERM_BP_ALL	glucose metabolism	

Supplemental Data Table S5. Continued.

GOTERM_BP_ALL	glutathione metabolism	
KEGG_PATHWAY	GLYCINE, SERINE AND THREONINE METABOLISM	
KEGG_PATHWAY	GLYCOLYSIS / GLUCONEOGENESIS	
KEGG_PATHWAY	GLYOXYLATE AND DICARBOXYLATE METABOLISM	
GOTERM_BP_ALL	heterocycle metabolism	
GOTERM_BP_ALL	hexose metabolism	
KEGG_PATHWAY	HISTIDINE METABOLISM	
KEGG_PATHWAY	LIMONENE AND PINENE DEGRADATION	
GOTERM_BP_ALL	lipid metabolism	
KEGG_PATHWAY	LYSINE DEGRADATION	
KEGG_PATHWAY	METABOLISM OF XENOBIOTICS BY CYTOCHROME P450	
GOTERM_BP_ALL	mitochondrial electron transport, NADH to ubiquinone	
GOTERM_BP_ALL	monosaccharide metabolism	
GOTERM_BP_ALL	nitrogen compound biosynthesis	
GOTERM_BP_ALL	nitrogen compound catabolism	
GOTERM_BP_ALL	nonprotein amino acid metabolism	
GOTERM_BP_ALL	nucleoside triphosphate biosynthesis	
GOTERM_BP_ALL	nucleotide biosynthesis	
KEGG_PATHWAY	ONE CARBON POOL BY FOLATE	
GOTERM_BP_ALL	one-carbon compound metabolism	
GOTERM_BP_ALL	organic anion transport	
GOTERM_BP_ALL	oxidative phosphorylation	
KEGG_PATHWAY	PANTOTHENATE AND COA BIOSYNTHESIS	
KEGG_PATHWAY	PROPANOATE METABOLISM	
GOTERM_BP_ALL	pteridine and derivative biosynthesis	
GOTERM_BP_ALL	purine ribonucleoside triphosphate biosynthesis	
GOTERM_BP_ALL	purine ribonucleotide biosynthesis	
KEGG_PATHWAY	PYRUVATE METABOLISM	
KEGG_PATHWAY	SELENOAMINO ACID METABOLISM	
GOTERM_BP_ALL	serine family amino acid biosynthesis	
GOTERM_BP_ALL	serine family amino acid catabolism	
SP_PIR_KEYWORDS	sodium transport	
GOTERM_BP_ALL	sulfur amino acid biosynthesis	
GOTERM_BP_ALL	sulfur amino acid catabolism	
GOTERM_BP_ALL	sulfur compound biosynthesis	
GOTERM_BP_ALL	sulfur compound catabolism	
SP_PIR_KEYWORDS	symport	
GOTERM_BP_ALL	tetrahydrobiopterin biosynthesis	
GOTERM_BP_ALL	transport	
GOTERM_BP_ALL	tricarboxylic acid cycle	
KEGG_PATHWAY	TRYPTOPHAN METABOLISM	
KEGG_PATHWAY	UREA CYCLE AND METABOLISM OF AMINO GROUPS	
KEGG_PATHWAY	VALINE, LEUCINE AND ISOLEUCINE DEGRADATION	
GOTERM_BP_ALL	water-soluble vitamin metabolism	

Supplemental Data Table S6. The Entire List of Pathways and the Change Direction of D-Serine-induced Differentially Expressed Genes Involved in Each of These Pathways under Various Categories as Determined Using GenMAPP.

Cellular Process			
Pathway	**Gene**	**Description**	
Apoptosis	Tnfrsf1a	Tumor necrosis factor receptor superfamily, member 1a	
	Nfkb1	Nuclear factor Kappa B p105 subunit	
	Casp8	Caspase-8	
	Casp2	Caspase 2	
	Mcl1	Myeloid cell leukemia sequence 1	
	Cys	Cytochrome c, somatic	
G1 to S cell cycle control	Cdk4	Cyclin-dependent kinase 4	
	Ccnh	Cyclin H	
	Mnat1	Menage a trois 1	
	Cdkn2c	Cyclin dependent kinase inhibitor 2C	
	Myc	v-myc avian myelocytomatosis viral oncogene homolog	
	E2f5	E2F transcription factor 5	
	Pcna	Proliferating cell nuclear antigen	
	Ccnd1	Cyclin D1	
GPCRs, Class B Secretin-like	Pthr1	Parathyroid hormone receptor 1	
MAPK Cascade	Map2k1	Mitogen activated protein kinase kinase 1	
	Map3k1	Mitogen activated protein kinase kinase kinase 1	
	Araf1	A-Raf proto-oncogene serine/threonine-protein kinase	
Eukaryotic Transcription Initiation	Taf9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor	
	Ccnh	Cyclin H	
	Mnat1	Menage a trois 1	
	Polr2g	Polymerase (RNA) II (DNA directed)polypeptide G	
Translations Factors	Eif3s7	Translation initiation factor eIF3 p66 subunit	
	Eif4ebp1	Eukaryotic translation initiation factor 4E binding protein 1	
	Pabpc1	Poly(A) binding protein, cytoplasmic 1	
	Ef1gamma	Similar to 2700038E08Rik protein	
	Eef1d	Translation elongation factor 1-delta subunit	
	Eef2	Elongation factor 2 (EF-2).	
Apoptosis Mechanisms	Tnfrsf1a	Tumor necrosis factor receptor superfamily, member 1a	
	Nfkb1	Nuclear factor kappa B p105 subunit	
	Map3k1	Mitogen activated protein kinase kinase kinase 1	
	Myc	v-myc avian myelocytomatosis viral oncogene homolog	
	Casp8	Caspase-8	
	Casp11	Caspase 11	
	Casp2	Caspase 2	
	Birc5	Baculoviral IAP repeat-containing protein 5 (Apoptosis inhibitor survivin)	
	Cycs	Cytochrome c, somatic	
Cell cycle	Madh4	MAD homolog 4 (Drosophila)	
	Cdk4	Cyclin-dependent kinase 4	
	AbL1	Abelson murine leukemia viral (v-abl) oncogene homolog 1	

Supplemental Data Table S6. Continued.

	Mcmd6	Mini chromosome maintenance deficient 6 (S. cerevisiae)
	Hdac1	Histone deacetylase 1
	E2f5	E2F transcription factor 5
	Tp53	Tumor protein p53 (Tumor suppressor p53)
	Pcna	Proliferating cell nuclear antigen
	Ccnh	Cyclin H
	Ywhag	Tyrosine 3-monooxgenase/tryptophan 5-monooxgenase activation protein, gamma polypeptide
	Chek1	Checkpoint kinase 1 (Cell cycle checkpoint protein kinase).
	Ccnb1	G2/mitotic-specific cyclin B1
	Plk	Serine/threonine-protein kinase PLK
	Pttg1	Pituitary tumor-transforming protein 1
	Cdc20	Cell cycle protein p55CDC
	Hdac6	Histone deacetylase 6
G13 Signaling Pathway	Arha2	Plysia ras-related homolog A2
	Cdc42	Cell division cycle 42 homolog (S. cerevisiae)
	Calm2	Calmodulin 2
	Rac1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
	Pfn1	Profilin
	Cfl1	Cofilin 1
Apoptosis Modulation by HSP70	Casp8	Caspase-8
	Map3k1	Mitogen activated protein kinase kinase kinase 1
	Casp2	Caspase 2
	Tnfrsf1a	Tumor necrosis factor receptor superfamily, member 1a
	Casp8	Caspase-8
	Nfkb1	Nuclear factor kappa B p105 subunit
	Cycs	Cytochrome c, somatic
mRNA processing (Mus Musculus)	Hnrpa1	Heterogeneous nuclear ribonucleoprotein A1
	Hnrpab	Heterogeneous nuclear ribonucleoprotein A/B
	Hnrpd	RNA binding protein p45AUF1
	Hnrpk	Heterogeneous nuclear ribonucleoprotein K
	Hnrpr	Heterogeneous nuclear ribonucleoprotein R
	Hnrpu	Transporter protein; system N1 Na+ and H+-coupled glutamine transporter
	Nsep1	Nuclease sensitive element binding protein 1
	Ppm1g	Protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform
	Sfrs10	Splicing factor, arginine/serine-rich (transformer 2 Drosophila homolog) 10
	Hrmt1l2	Protein arginine N-methyltransferase 1
Signal Transduction of S1 Receptor	Akt1	v-akt murine thymoma viral oncogene homolog 1
	Gnai2	GTP-binding protein (G-alpha-i2)
Wnt Signaling Pathway	Fzd2	Frizzled 2 precursor (Frizzled-2)
	Arha2	Plysia ras-related homolog A2
	Ccnd1	Cyclin D1
DNA Replication	Mcm3	Similar to DNA replication licensing factor MCM3 (DNA polymerase alpha holoenzyme-associated protein P1) (P1-MCM3
	Pcna	Proliferating cell nuclear antigen

Supplemental Data Table S6. Continued.

G Protein Signaling Pathways	Akap12	A kinase (PRKA) anchor protein (gravin) 12	
	Gnb1	Guanine nucleotide binding protein, beta 1	
	Gnb2	Guanine nucleotide binding protein, beta polypeptide 2	
	Gnai2	GTP-binding protein (G-alpha-i2)	
	Prkar1a	Protein kinase, cAMP dependent regulatory, type I, alpha	
	Arha2	Plysia ras-related homolog A2	
	Ppp3cb	Protein phosphatase 3, catalytic subunit, beta isoform	
	Calm2	calmodulin 2	
	Prkcb1	Protein kinase C, beta 1	
	Prkar2a	Protein kinase, cAMP-dependent, regulatory, type 2, alpha	
Integrin-mediated cell adhesion	Capns1	Calpain, small subunit 1	
	Rap1b	RAP1B, member of RAS oncogene family	
	Cdc42	Cell division cycle 42 homolog (S. cerevisiae)	
	Rac1	Ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	
	Akt1	v-akt murine thymoma viral oncogene homolog 1	
	Map2k1	Mitogen activated protein kinase kinase 1	
	Araf1	v-raf murine sarcoma 3611 viral oncogene homolog 1	
	Sepp1	Selenoprotein P precursor (SeP).	
Regulation of actin cytoskeleton	Nras	Neuroblastoma RAS viral (v-ras) oncogene homolog	
	Map2k1	Mitogen activated protein kinase kinase 1	
	F2r	Coagulation factor II receptor	
	Cd14	CD14 antigen	
	Actn1	Actinin, alpha 1	
	Actb	Actin, beta	
	Map2k1	Mitogen activated protein kinase kinase 1	
	F2r	Coagulation factor II receptor	
	Cd14	CD14 antigen	
	Pfn1	Profilin	
	Fn1	Fibronectin 1	
	Itga1	Integrin alpha 1	
	Rac1	Ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	
	Pak2	p21 (CDKN1A)-activated kinase 2	
	Cfl1	Cofilin 1	
	Abi2	Abl-interactor 2	
	Actb	Actin, beta	
	Tmsb4x	Thymosin beta-4	
	Egfr	Epidermal growth factor receptor	
	Fgfr1	Fibroblast growth factor receptor 1	
	F2	Coagulation factor 2	
TGF-beta signaling pathway	Fkbp1a	FK506-binding protein 1a	
	Madh1	Mothers against decapentaplegic homolog 1	
	Nfkb1	Nuclear factor kappa B p105 subunit	
	Madh4	Mothers against decapentaplegic homolog 4 (	
	Spp1	Secreted phosphoprotein 1	
	Stat3	Signal transducer and activator of transcription 3	
	Bmp4	Bone morphogenetic protein 4	

Supplemental Data Table S6. Continued.

Metabolic Process			
Pathway	**Gene**	**Description**	
Cholesterol Biosynthesis	Fdft1	farnesyl diphosphate farnesyl transferase 1	
Electron Transport Chain	Ndufv2	24-kDa subunit of mitochondrial NADH dehydrogenase	
	Cycs	Cytochrome c, somatic.	
	Cox5b	Cytochrome c oxidase polypeptide Vb, mitochondrial precursor	
	Cox6a1	Cytochrome c oxidase polypeptide VIa-liver, mitochondrial precursor	
	Cox7a3	Cytochrome c oxidase, subunit 7a 3	
	Cox8a	Cytochrome c oxidase, subunit VIIIa	
	Atp5a1	Mitochondrial H+-ATP synthase alpha subunit	
	Atp5b	ATP synthase beta chain, mitochondrial precursor	
	Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	
	Atp5o	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	
	Slc25a5	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	
	Ucp2	Mitochondrial uncoupling protein 2 (UCP 2).	
Glucocorticoid Metabolism	Hsd11b1	Hydroxysteroid 11-beta dehydrogenase 1	
Heme Biosyntesis	Alad	Delta-aminolevulinic acid dehydratase	
Pentose Phosphate Pathway	G6pdx	Glucose-6-phosphate dehydrogenase	
	Tkt	Transketolase	
Steroid Biosynthesis	Hsd17b4	Peroxisomal multifunctional enzyme type II.	
Acetylcholine Synthesis	Pdha1	Pyruvate dehydrogenase E1 component alpha subunit, somatic form, mitochondrial precursor	
Fatty Acid Degradation	Facl5	Fatty acid Coenzyme A ligase, long chain 5	
	Crat	Similar to carnitine acetyltransferase	
	Acads	Short chain acyl-coenzyme A dehydrogenase	
	Acadm	Acetyl-coenzyme A dehydrogenase, medium chain	
Glycogen Metabolism	Ppp3cb	Protein phosphatase 3, catalytic subunit, beta isoform	
	Gyg	Glycogenin	
	Pgm1	Phosphoglucomutase 1	
	Ppp2ca	Protein phosphatase 2a, catalytic subunit, alpha isoform	
TCA Cycle	Mdh1	Cytoplasmic malate dehydrogenase	
	Pc	Pyruvate carboxylase, mitochondrial precursor	
	Sdhd	Succinate dehydrogenase complex, subunit D, integral membrane protein	
	Pdha1	Pyruvate dehydrogenase E1 component alpha subunit, somatic form, mitochondrial precursor	
	Aco2	Mitochondrial aconitase precursor.	
	IDH3B	NAD+-specific isocitrate dehydrogenase b subunit	
	Idh3g	Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial precursor	
	Af6	Afadin	

Supplemental Data Table S6. Continued.

Prostaglandin Synthesis and Regulation	S100a10	S-100 related protein, clone 42C	
	Anxa1	Annexin 1	
	Anxa2	Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (Chromobindin 8) (P36) (Protein I) (Placental anticoagulant protein IV)	
	Anxa4	Annexin A4 (Annexin IV) (Lipocortin IV) (36 kDa zymogen granule membrane associated protein) (ZAP36).	
	Anxa5	Annexin 5	
	Hsd11b1	Hydroxysteroid 11-beta dehydrogenase 1	
Synthesis and Degradation of Ketone Bodies (HMG-CoA cycle)	Hmgcl	Hydroxymethylglutaryl-CoA lyase, mitochondrial precursor	
Boigenic Amine Synthesis	Maoa	Monoamine oxidase A	
Eicosanoid Synthesis	Tgm2	Tissue-type transglutaminase	
	Pla2g6	Phospholipase A2, group VI	
Fatty Acids Synthesis	Prkab1	Protein kinase, AMP-activated, beta 1 non-catalytic subunit	
	Acly	ATP-citrate synthase	
	Pc	Pyruvate carboxylase	
	Prkaa2	AMP-activated protein kinase	
	Echs1	Enoyl Coenzyme A hydratase, short chain 1	
	Scd1	Stearoyl-Coenzyme A desaturase 1	
Glycolysis and Gluconeogenesis	Aldoa	Aldolase A	
	Gapd	Glyceraldehyde-3-phosphate dehydrogenase	
	Pkm2	Pyruvate kinase, muscle	
	Ldha	Lactate dehydrogenase A	
	Fbp1	Fructose-1,6- biphosphatase 1	
	Aldob	Aldolase B	
	Pklr	Pyruvate kinase, liver and RBC	
	Mdh1	Malate dehydrogenase 1	
	Pc	Pyruvate carboxylase	
	PDHA1	Pyruvate dehydrogenase E1 component alpha subunit, somatic form, mitochondrial precursor	
Mitochondrial LC-Fatty Acid Beta-Oxidation	Facl5	Fatty acid Coenzyme A ligase, long chain 5	
	Acadm	Acetyl-coenzyme A dehydrogenase, medium chain	
	Acads	Acyl-CoA dehydrogenase, short-chain specific, mitochondrial precursor	
	Echs1	Enoyl Coenzyme A hydratase, short chain 1	
Statin Pathway (Pharm GKB)	Soat1	Sterol O-acyltransferase 1	
	Apoc3	Apolipoprotein C-III	
Molecular Function			
Pathway	**Gene**	**Description**	
Nuclear Receptors	Thrb	Thyroid hormone receptor beta	

Supplemental Data Table S6. Continued.

	Hnf4a	Hepatocyte nuclear factor 4, alpha	
	Nr1h3	Nuclear receptor subfamily 1, group H, member 3	
GPCRs, Class B Secretin-Like	Pthr1	Parathyroid hormone receptor 1	
Peptide GPCRs	Gnrhr	Gonadotropin-releasing hormone receptor	
Matrix Metalloproteinases	Mmp2	Matrix metalloproteinase 2 (72 KDa type IV collagenase)	
	Timp1	Metalloproteinase inhibitor 1 precursor (TIMP-1).	
	Timp2	Metalloproteinase inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of metalloproteinases-2).	
	Mmp14	Matrix metalloproteinase 14, membrane-inserted	
	Mmp24	Matrix metalloproteinase 24 (membrane-inserted)	
Cytoplasmic Ribosomal Proteins	Rpl4	60S ribosomal protein L4	
	Rpl5	60S ribosomal protein L5.	
	Rpl6	60S ribosomal protein L6	
	Rp17	60S ribosomal protein L7.	
	Rpl8	60S ribosomal protein L8.	
	Rpl10a	60S ribosomal protein L10a	
	Rpl13	60S ribosomal protein L13.	
	Rpl14	60S ribosomal protein L14	
	Rpl15	60S ribosomal protein L15.	
	Rpl17	60S ribosomal protein L17	
	Rpl18	60S ribosomal protein L18.	
	Rpl22	60S ribosomal protein L22.	
	Rpl23	60S ribosomal protein L23	
	Rpl24	60S ribosomal protein L24	
	Rpl28	60S ribosomal protein L28.	
	Rpl29	60S ribosomal protein L29	
	Rpl30	60S ribosomal protein L30	
	Rpl31	60S ribosomal protein L31	
	Rpl32	60S ribosomal protein L32	
	Rpl35a	60S ribosomal protein L35a	
	Rpl37	60S ribosomal protein L37	
	Arbp	60S acidic ribosomal protein P0	
	Rplp2	60S acidic ribosomal protein P2	
	Lamr1	40S ribosomal protein SA	
	Rps2	Ribosomal protein S2	
	Rps3	40S ribosomal protein S3	
	Rps4x	40S ribosomal protein S4, X isoform	
	Rps5	40S ribosomal protein S5	
	Rps6	40S ribosomal protein S6	
	Rps7	40S ribosomal protein S7	
	Rps8	40S ribosomal protein S8	
	Rps9	40S ribosomal protein S9	
	Rps10	40S ribosomal protein S10	
	Rps12	40S ribosomal protein S12	
	Rps13	40S ribosomal protein S13	
	Rps14	40S ribosomal protein S14	
	Rps15	40S ribosomal protein S15	

Supplemental Data Table S6. Continued.

	Rps15a	40S ribosomal protein S15a	
	Rps17	40S ribosomal protein S17	
	Rps19	40S ribosomal protein S19	
	Rps20	40S ribosomal protein S20	
	Rps21	40S ribosomal protein S21	
	Rps24	40S ribosomal protein S24	
	Rps26	40S ribosomal protein S26	
	Rps27a	40S ribosomal protein S27a	
Physiological Process			
Pathway	**Gene**	**Description**	
Calcium Regulation in the Cardiac Cell	Fkbp1a	FK506-binding protein 1A	
	Gja1	Gap junction alpha-1 protein	
	Itpr3	Inositol 1,4,5-trisphosphate receptor type 3	
	Prkar1a	cAMP-dependent protein kinase type I-alpha regulatory chain	
	Camk2d	Calcium/calmodulin-dependent protein kinase type II delta chain	
	Calm1	Calmodulin 1	
	Calm2	Calmodulin 2	
	Gnb1	Guanine nucleotide-binding protein, beta subunit 1	
	Gnb2	Guanine nucleotide binding protein, beta polypeptide 2	
	Gnai2	GTP-binding protein (G-alpha-i2)	
	Rgs3	Regulator of G-protein signaling 3	
	Ywhab	Tyrosine 3-monooxgenase/tryptophan 5 monooxgenase activation protein, beta polypeptide	
	Ywhae	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	
	Ywhah	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	
	Ywhag	Tyrosine 3-monooxgenase/tryptophan 5-monooxgenase activation protein, gamma polypeptide	
	Ywhaq	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	
	Ywhaz	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	
	Fxyd2	FXYD domain-containing ion transport regulator 2	
	Prkar2a	Protein kinase, cAMP-dependent, regulatory, type 2, alpha	
Inflammatory Response Pathway	Tnfrsf1a	Tumor necrosis factor receptor superfamily member 1A precursor	
	Fn1	Fibronectin 1	
	Lama5	Laminin, alpha 5	
	Lamc1	Laminin, gamma 1	
	Mmp2	Matrix metalloproteinase 2 (72 KDa type IV collagenase)	
	Col3a1	Collagen, type III, alpha 1	
	Col1a2	Procollagen, type I, alpha 2	
Myometrial Relaxation and Contraction Pathways	Gnb1	Guanine nucleotide binding protein, beta 1	
	Gnb2	Guanine nucleotide binding protein, beta polypeptide 2	
	Prkar1a	cAMP-dependent protein kinase type I-alpha regulatory chain	
	Igfbp6	Insulin-like growth factor binding protein 6	
	Ramp2	Receptor (calcitonin) activity modifying protein 2	
	Actb	Beta-actin FE-3	
	Nfkb1	Nuclear factor NF-kappa-B p105 subunit	

Supplemental Data Table S6. Continued.

	Gja1	Gap junction alpha-1 protein
	Rgs3	Regulator of G-protein signaling 3
	Ywhab	Tyrosine 3-monooxgenase/tryptophan 5 monooxgenase activation protein, beta polypeptide
	Ywhae	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide
	Ywhah	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
	Ywhag	Tyrosine 3-monooxgenase/tryptophan 5-monooxgenase activation protein, gamma polypeptide
	Ywhaq	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide
	Ywhaz	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
	Itpr3	Inositol 1,4,5-trisphosphate receptor type 3
	Calm1	Calmodulin 1
	Calm2	Calmodulin 2
	Camk2d	Calcium/calmodulin-dependent protein kinase type II delta chain
	Prkar2a	cAMP-dependent protein kinase type II-alpha regulatory chain
	Guca2b	Uroguanylin precursor (UGN) (Guanylate cyclase activator 2B).
ACE Inhibitor Pathway	Agt	Angiotensinogen
	Ace	Angiotensin-converting enzyme
Complement Activation, Classical Pathway	C7	Complement component 7
Oxidative Stress	Nfkb1	Nuclear factor NF-kappa-B p105 subunit
	Maoa	Monoamine oxidase A
	Cat	Catalase
	Gclc	Glutamate-cysteine ligase catalytic subunit
	Gstt2	Glutathione S-transferase, theta 2
	Sod1	Superoxide dismutase 1
Striated Muscle Contraction	Tpm1	Tropomyosin 1, alpha
	Tpm3	Tropomyosin 3, gamma
	Tpm4	Tropomyosin alpha 4 chain
	Vim	Vimentin
Blood Clotting Cascade	Plat	Tissue-type plasminogen activator precursor
	Vwf	Von Willebrand factor
	F2	Coagulation factor 2
Complement Activation, Classical Pathway	A2m	Alpha-2-macroglobulin precursor
	F2r	Coagulation factor II receptor
	Plat	Tissue-type plasminogen activator precursor
	Crry	Complement receptor related protein
	C7	Complement component 7
	Vwf	Von Willebrand factor
	Proc	Vitamin-K-dependent protein C precursor
	F2	Coagulation factor 2
	Serping1	serine (or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1, (angioedema, hereditary)

Supplemental Data Table S6. Continued.

Proteasome Degradation	H2afz	H2A histone family, member Z	
	Rpn1	Ribophorin I	
	Psmc3	Proteasome (prosome, macropain) 26S subunit, ATPase 3	
	Ube2n	Ubiquitin-conjugating enzyme E2N	
	Nedd4a	Neural precursor cell expressed, developmentally down-regulated gene 4A	
	Psma1	Proteasome subunit alpha type 1	
	Psma2	Proteasome subunit alpha type 2	
	Psma5	Proteasome subunit alpha type 5	
	Psmb4	Proteasome subunit beta type 4 precursor	
	Psmb8	Proteasome subunit beta type 8 precursor	
	Psmb9	Proteasome subunit beta type 9 precursor	
	Psmb10	Proteasome subunit beta type 10 precursor	
	Psme1	Proteasome activator complex subunit 1	
	Psme2	Proteasome activator complex subunit 2	

Supplemental Data Table S7. The Entire List of D-Serine-induced Differentially Expressed Genes and Their Changes Direction Involved in Biological Association Networks of Promoter Binding, Regulation, Transport, Protein Modification, Expression, and Binding as Determined Using PathwayArchitect.

Promoter Binding Network		
Gene	**Gene Description**	**Change Direction**
A2M	alpha-2-macroglobulin	up
CNTF	ciliary neurotrophic factor	up
COL1A1	collagen, type I, alpha 1	up
COL1A2	collagen, type I, alpha 2	up
EGR1	early growth response 1	up
FBN1	fibrillin 1 (Marfan syndrome)	up
FN1	fibronectin 1	up
GJA1	gap junction protein, alpha 1, 43kDa (connexin 43)	up
HNRPK	heterogeneous nuclear ribonucleoprotein K	up
IRF-1	interferon regulatory factor 1	up
LDHA	lactate dehydrogenase A	up
LMNA	lamin A/C	up
MMP2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	up
MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	up
NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	up
PCNA	proliferating cell nuclear antigen	up
PSMB8	proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7)	up
PSMB9	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional peptidase 2)	up
PTBP1	polypyrimidine tract binding protein 1	up
PTTG1	pituitary tumor-transforming 1	up
RPL3	ribosomal protein L3	up
SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	up
SOAT1	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	up
SPP1	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	up
TGFBR2	transforming growth factor, beta receptor II (70/80kDa)	up
TIMP1	TIMP metallopeptidase inhibitor 1	up
TK1	thymidine kinase 1, soluble	up
TP53	tumor protein p53 (Li-Fraumeni syndrome)	up
VIM	vimentin	up
CBS	cystathionine-beta-synthase	down
CCND1	cyclin D1 (PRAD1: parathyroid adenomatosis 1)	down
DHFR	dihydrofolate reductase	down
EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	down

Supplemental Data Table S7.
Transport, Protein Modification, Expression, and Binding as Determined Using PathwayArchitect.

GC	group-specific component (vitamin D binding protein)	down
GHR	growth hormone receptor	down
HNF4A	hepatocyte nuclear factor 4, alpha	down
NEF3	neurofilament 3 (150kDa medium)	down
NR1H3	nuclear receptor subfamily 1, group H, member 3	down
Nt5	5 nucleotidase	down
ODC1	ornithine decarboxylase 1	down
ROS1	v-ros UR2 sarcoma virus oncogene homolog 1 (avian)	down
Regulation Network		
Gene	**Gene Description**	**Change direction**
ACTB	actin, beta	up
ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	up
AKT1	v-akt murine thymoma viral oncogene homolog 1	up
ANXA1	annexin A1	up
ARSB	arylsulfatase B	up
AVPI1	arginine vasopressin-induced 1	up
B4GALT1	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	up
BGN	biglycan	up
CALM1	calmodulin 1 (phosphorylase kinase, delta)	up
CASP3	caspase 3, apoptosis-related cysteine peptidase	up
CCNB1	cyclin B1	up
CD151	CD151 antigen	up
CD9	CD9 antigen (p24)	up
CDW92	CDW92 antigen	up
COL3A1	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	up
CSPG6	chondroitin sulfate proteoglycan 6 (bamacan)	up
CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	up
EEF2	eukaryotic translation elongation factor 2	up
EGR1	early growth response 1	up
FN1	fibronectin 1	up
GM2A	GM2 ganglioside activator	up
GSTM1	glutathione S-transferase M1	up
GUSB	glucuronidase, beta	up
H2AFY	H2A histone family, member Y	up
HAVCR1	hepatitis A virus cellular receptor 1	up
IL1RL1	interleukin 1 receptor-like 1	up
KPNB1	karyopherin (importin) beta 1	up
Krt2-8	keratin complex 2, basic, gene 8	up
Lamr1	laminin receptor 1 (67kD, ribosomal protein SA)	up
LDHA	lactate dehydrogenase A	up
Ler3	immediate early response 3	up
LGALS3	lectin, galactoside-binding, soluble, 3 (galectin 3)	up
LIG1	ligase I, DNA, ATP-dependent	up

Supplemental Data Table S7. Continued.

LMNA	lamin A/C	up
MAOA	monoamine oxidase A	up
MAP2K1	mitogen-activated protein kinase kinase 1	up
MAP3K1	mitogen-activated protein kinase kinase kinase 1	up
MAPRE1	microtubule-associated protein, RP/EB family, member 1	up
MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	up
MMP2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	up
MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	up
MYO1B	myosin IB	up
NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	up
NPM1	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	up
PFN1	profilin 1	up
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	up
PLAT	plasminogen activator, tissue	up
PPM1G	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	up
PPP1CA	protein phosphatase 1, catalytic subunit, alpha isoform	up
PPP1R14B	protein phosphatase 1, regulatory (inhibitor) subunit 14B	up
PRDX2	peroxiredoxin 2	up
PRKCB1	protein kinase C, beta 1	up
PRKCDBP	protein kinase C, delta binding protein	up
PSMA2	proteasome (prosome, macropain) subunit, alpha type, 2	up
PTPN2	protein tyrosine phosphatase, non-receptor type 2	up
PYCARD	PYD and CARD domain containing	up
RHOA	ras homolog gene family, member A	up
S100A4	S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog)	up
SCARB1	scavenger receptor class B, member 1	up
SDCBP	syndecan binding protein (syntenin)	up
SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	up
SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	up
SLK	STE20-like kinase (yeast)	up
SPARC	secreted protein, acidic, cysteine-rich (osteonectin)	up
SPP1	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	up
SUMO2	SMT3 suppressor of mif two 3 homolog 2 (yeast)	up
TCP1	t-complex 1	up
TIMP1	TIMP metallopeptidase inhibitor 1	up
TK1	thymidine kinase 1, soluble	up

Supplemental Data Table S7. Continued.

TKT	transketolase (Wernicke-Korsakoff syndrome)	up
TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A	up
TP53	tumor protein p53 (Li-Fraumeni syndrome)	up
TPM3	tropomyosin 3	up
TUBB2	tubulin, beta 2	up
UBD	ubiquitin D	up
VIM	vimentin	up
YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	up
ACE	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	down
AGT	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	down
AHCY	S-adenosylhomocysteine hydrolase	down
AK3	adenylate kinase 3	down
APOC3	apolipoprotein C-III	down
Araf1	v-raf oncogene homolog 1 (murine sarcoma 3611 virus)	down
BCKDHB	branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease)	down
CAT	catalase	down
Cml1	camello-like 1	down
CRYAB	crystallin, alpha B	down
DPP4	dipeptidylpeptidase 4 (CD26, adenosine deaminase complexing protein 2)	down
EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	down
ENPP3	ectonucleotide pyrophosphatase/phosphodiesterase 3	down
EPHX2	epoxide hydrolase 2, cytoplasmic	down
GC	group-specific component (vitamin D binding protein)	down
GGT1	gamma-glutamyltransferase 1	down
GSTA5	glutathione S-transferase A5	down
HNMT	histamine N-methyltransferase	down
MAPT	microtubule-associated protein tau	down
MDH1	malate dehydrogenase 1, NAD (soluble)	down
ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	down
Naglt1	Na+ dependent glucose transporter 1	down
NFS1	NFS1 nitrogen fixation 1 (S. cerevisiae)	down
NIT1	nitrilase 1	down
ODC1	ornithine decarboxylase 1	down
PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	down
PLA2G6	phospholipase A2, group VI (cytosolic, calcium-independent)	down
PPP1R1B	protein phosphatase 1, regulatory (inhibitor) subunit 1B (dopamine and cAMP regulated phosphoprotein, DARPP-32)	down
PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha	down

Supplemental Data Table S7. Continued.

PTHR1	parathyroid hormone receptor 1	down
PTS	6-pyruvoyltetrahydropterin synthase	down
RGN	regucalcin (senescence marker protein-30)	down
ROS1	v-ros UR2 sarcoma virus oncogene homolog 1 (avian)	down
SLC19A1	solute carrier family 19 (folate transporter), member 1	down
SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	down
SLC34A1	solute carrier family 34 (sodium phosphate), member 1	down
SOD1	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	down
THRB	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	down
TYRO3	TYRO3 protein tyrosine kinase	down
VWF	von Willebrand factor	down
Transport Network		
Gene	**Gene Description**	**Change direction**
A2M	alpha-2-macroglobulin	up
ABL1	v-abl Abelson murine leukemia viral oncogene homolog 1	up
AKT1	v-akt murine thymoma viral oncogene homolog 1	up
ALDOA	aldolase A, fructose-bisphosphate	up
ANXA1	annexin A1	up
ARF6	ADP-ribosylation factor 6	up
AVPI1	arginine vasopressin-induced 1	up
BGN	biglycan	up
BZRP	benzodiazapine receptor (peripheral)	up
CA3	carbonic anhydrase III, muscle specific	up
CALM1	calmodulin 1 (phosphorylase kinase, delta)	up
CASP3	caspase 3, apoptosis-related cysteine peptidase	up
COL1A1	collagen, type I, alpha 1	up
DAG1	dystroglycan 1 (dystrophin-associated glycoprotein 1)	up
DAP	death-associated protein	up
DPYSL3	dihydropyrimidinase-like 3	up
EEF2	eukaryotic translation elongation factor 2	up
EGR1	early growth response 1	up
F2R	coagulation factor II (thrombin) receptor	up
FKBP1A	FK506 binding protein 1A, 12kDa	up
FN1	fibronectin 1	up
FZD2	frizzled homolog 2 (Drosophila)	up
GJA1	gap junction protein, alpha 1, 43kDa (connexin 43)	up
GM2A	GM2 ganglioside activator	up
IL1RL1	interleukin 1 receptor-like 1	up
LDHA	lactate dehydrogenase A	up
LGALS1	lectin, galactoside-binding, soluble, 1 (galectin 1)	up
MAOA	monoamine oxidase A	up

Supplemental Data Table S7. Continued.

MAP2K1	mitogen-activated protein kinase kinase 1	up
Mgl1	macrophage galactose N-acetyl-galactosamine specific lectin 1	up
MGP	matrix Gla protein	up
Mlp	MARCKS-like protein	up
MMP2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	up
MTPN	myotrophin	up
MYO1B	myosin IB	up
NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	up
NPC2	Niemann-Pick disease, type C2	up
PFN1	profilin 1	up
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	up
Pkcl	protein kinase C, lambda	up
PLAT	plasminogen activator, tissue	up
PRKCB1	protein kinase C, beta 1	up
PTPN2	protein tyrosine phosphatase, non-receptor type 2	up
PYCARD	PYD and CARD domain containing	up
RHOA	ras homolog gene family, member A	up
RNH1	ribonuclease/angiogenin inhibitor 1	up
RPS6	ribosomal protein S6	up
SCARB1	scavenger receptor class B, member 1	up
SLC10A2	solute carrier family 10 (sodium/bile acid cotransporter family), member 2	up
SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	up
SLK	STE20-like kinase (yeast)	up
SOAT1	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	up
TAF9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	up
TIMP2	TIMP metallopeptidase inhibitor 2	up
TP53	tumor protein p53 (Li-Fraumeni syndrome)	up
TPM1	tropomyosin 1 (alpha)	up
VIM	vimentin	up
YWHAE	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	up
YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	up
ACE	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	down
AFM	afamin	down
AGT	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	down
ANPEP	alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)	down

Supplemental Data Table S7. Continued.

APOC3	apolipoprotein C-III	down
CAT	catalase	down
CYCS	cytochrome c, somatic	down
DCXR	dicarbonyl/L-xylulose reductase	down
EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	down
ENPEP	glutamyl aminopeptidase (aminopeptidase A)	down
ENPP3	ectonucleotide pyrophosphatase/phosphodiesterase 3	down
F2	coagulation factor II (thrombin)	down
FBP1	fructose-1,6-bisphosphatase 1	down
FXYD2	FXYD domain containing ion transport regulator 2	down
GC	group-specific component (vitamin D binding protein)	down
GHR	growth hormone receptor	down
GSTA2	glutathione S-transferase A2	down
GUCA2B	guanylate cyclase activator 2B (uroguanylin)	down
MLYCD	malonyl-CoA decarboxylase	down
NR1H3	nuclear receptor subfamily 1, group H, member 3	down
PC	pyruvate carboxylase	down
PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	down
PKLR	pyruvate kinase, liver and RBC	down
PLA2G6	phospholipase A2, group VI (cytosolic, calcium-independent)	down
PRKAA2	protein kinase, AMP-activated, alpha 2 catalytic subunit	down
PRSS8	protease, serine, 8 (prostasin)	down
RBP4	retinol binding protein 4, plasma	down
RGN	regucalcin (senescence marker protein-30)	down
SCP2	sterol carrier protein 2	down
Sdhb_predicted	succinate dehydrogenase complex, subunit B, iron sulfur (Ip) (predicted)	down
SLC13A3	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	down
SLC1A1	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	down
SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	down
SLC34A1	solute carrier family 34 (sodium phosphate), member 1	down
SLC38A3	solute carrier family 38, member 3	down
SLC3A1	solute carrier family 3 (cystine, dibasic and neutral amino acid transporters, activator of cystine, dibasic and neutral amino acid transport), member 1	down
SOD1	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))	down
TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	down
VWF	von Willebrand factor	down

Supplemental Data Table S7. Continued.

Protein Modification Network		
Gene	**Gene Description**	**Change direction**
ABL1	v-abl Abelson murine leukemia viral oncogene homolog 1	up
ACLY	ATP citrate lyase	up
ACTB	actin, beta	up
AKAP1	A kinase (PRKA) anchor protein 1	up
AKT1	v-akt murine thymoma viral oncogene homolog 1	up
ANXA1	annexin A1	up
ANXA2	annexin A2	up
CALD1	caldesmon 1	up
CALM1	calmodulin 1 (phosphorylase kinase, delta)	up
CAMK2D	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta	up
CCNB1	cyclin B1	up
CD81	CD81 antigen (target of antiproliferative antibody 1)	up
CFL1	cofilin 1 (non-muscle)	up
CSNK2B	casein kinase 2, beta polypeptide	up
CUTL1	cut-like 1, CCAAT displacement protein (Drosophila)	up
EEF2	eukaryotic translation elongation factor 2	up
EGR1	early growth response 1	up
EIF4A1	eukaryotic translation initiation factor 4A, isoform 1	up
EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1	up
F2R	coagulation factor II (thrombin) receptor	up
FGFR2	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome)	up
GNAI2	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	up
JAK3	Janus kinase 3 (a protein tyrosine kinase, leukocyte)	up
KHDRBS1	KH domain containing, RNA binding, signal transduction associated 1	up
Madh4	MAD homolog 4 (Drosophila)	up
MAP3K1	mitogen-activated protein kinase kinase kinase 1	up
Mlp	MARCKS-like protein	up
MMP2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	up
MTPN	myotrophin	up
MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	up
NCL	nucleolin	up
NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	up
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	up
PKM2	pyruvate kinase, muscle	up
PTPNS1	protein tyrosine phosphatase, non-receptor type	up

Supplemental Data Table S7. Continued.

	substrate 1	
RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	up
RAN	RAN, member RAS oncogene family	up
RAP1B	RAP1B, member of RAS oncogene family	up
RHOA	ras homolog gene family, member A	up
RNH1	ribonuclease/angiogenin inhibitor 1	up
RPS27A	ribosomal protein S27a	up
SLK	STE20-like kinase (yeast)	up
SMAD1	SMAD, mothers against DPP homolog 1 (Drosophila)	up
SOAT1	sterol O-acyltransferase (acyl-Coenzyme A: cholesterol acyltransferase) 1	up
STAT3	signal transducer and activator of transcription 3 (acute-phase response factor)	up
STX4A	syntaxin 4A (placental)	up
TIMP1	TIMP metallopeptidase inhibitor 1	up
TP53	tumor protein p53 (Li-Fraumeni syndrome)	up
Tph	tryptophan hydroxylase	up
TUBA1	tubulin, alpha 1 (testis specific)	up
TUBB2	tubulin, beta 2	up
VIM	vimentin	up
YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	up
BMP4	bone morphogenetic protein 4	down
EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	down
ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	down
FAH	fumarylacetoacetate hydrolase (fumarylacetoacetase)	down
HMGCL	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase (hydroxymethylglutaricaciduria)	down
MAPT	microtubule-associated protein tau	down
MME	membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)	down
NEF3	neurofilament 3 (150kDa medium)	down
PPP1R1B	protein phosphatase 1, regulatory (inhibitor) subunit 1B (dopamine and cAMP regulated phosphoprotein, DARPP-32)	down
PPP2CA	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	down
RGN	regucalcin (senescence marker protein-30)	down
ROS1	v-ros UR2 sarcoma virus oncogene homolog 1 (avian)	down
SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	down
TNXA	tenascin XA pseudogene	down
Expression Network		
Gene	**Gene Description**	**Change direction**

Supplemental Data Table S7. Continued.

AKT1	v-akt murine thymoma viral oncogene homolog 1	up
CD44	CD44 antigen (homing function and Indian blood group system)	up
CEBPD		up
COL1A1	collagen, type I, alpha 1	up
COL3A1	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	up
EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1	up
FN1	fibronectin 1	up
GUSB	glucuronidase, beta	up
HN1	hematological and neurological expressed 1	up
HRMT1L2	HMT1 hnRNP methyltransferase-like 2 (S. cerevisiae)	up
LEPRE1	leucine proline-enriched proteoglycan (leprecan) 1	up
MAF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	up
MAP2K1	mitogen-activated protein kinase kinase 1	up
MGP	matrix Gla protein	up
MMP2	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	up
MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	up
NUP62	nucleoporin 62kDa	up
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (p85 alpha)	up
PKM2	pyruvate kinase, muscle	up
PPM1G	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	up
PRKCB1	protein kinase C, beta 1	up
PTMA	prothymosin, alpha (gene sequence 28)	up
SDCBP	syndecan binding protein (syntenin)	up
SPP1	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1)	up
TIMP1	TIMP metallopeptidase inhibitor 1	up
TNC	tenascin C (hexabrachion)	up
TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A	up
TP53	tumor protein p53 (Li-Fraumeni syndrome)	up
TUBA1	tubulin, alpha 1 (testis specific)	up
UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	up
YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	up
ANPEP	alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150)	down
EGFR	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	down
ETFA	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)	down

Supplemental Data Table S7. Continued.

GPX4	glutathione peroxidase 4 (phospholipid hydroperoxidase)	down
GSTA5	glutathione S-transferase A5	down
PTHR1	parathyroid hormone receptor 1	down
SDC2	syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)	down
SKP1A	S-phase kinase-associated protein 1A (p19A)	down
Binding Network		
Gene	**Gene Description**	**Change direction**
A2M	alpha-2-macroglobulin	up
ACTB	actin, beta	up
ADAMTS1	ADAM metallopeptidase with thrombospondin type 1 motif, 1	up
AKT1	v-akt murine thymoma viral oncogene homolog 1	up
CCT5	chaperonin containing TCP1, subunit 5 (epsilon)	up
CDC42	cell division cycle 42 (GTP binding protein, 25kDa)	up
COL3A1	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)	up
CSPG6	chondroitin sulfate proteoglycan 6 (bamacan)	up
CTSC	cathepsin C	up
CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	up
HNRPK	heterogeneous nuclear ribonucleoprotein K	up
MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	up
MYO1B	myosin IB	up
NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)	up
NPDC1	neural proliferation, differentiation and control, 1	up
NUP62	nucleoporin 62kDa	up
PRKCDBP	protein kinase C, delta binding protein	up
PTPNS1	protein tyrosine phosphatase, non-receptor type substrate 1	up
RAC1	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	up
RAP1B	RAP1B, member of RAS oncogene family	up
RPS27A	ribosomal protein S27a	up
SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	up
SSB	Sjogren syndrome antigen B (autoantigen La)	up
TP53	tumor protein p53 (Li-Fraumeni syndrome)	up
YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	up
ACE	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	down
ACO1	aconitase 1, soluble	down
FDFT1	farnesyl-diphosphate farnesyltransferase 1	down
PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	down
TAS1R2	taste receptor, type 1, member 2	down
VWF	von Willebrand factor	down

Supplemental Data Table S8. The Affymetrix ID, Name/Description and Change Direction of Differentially Expressed Genes in the Kidney after PUR Exposure Commonly Identified Using ANOVA and SAM.

AFFY_ID	Gene Name	Direction
1367462_at	calpain, small subunit 1	Up
1367464_at	siah binding protein 1; fbp interacting repressor; pyrimidine tract binding splicing factor; ro ribonucleoprotein-binding protein 1	Up
1367473_at	translocase of outer mitochondrial membrane 22 homolog (yeast)	Up
1367475_at	cell division cycle 42 homolog (s. cerevisiae)	Up
1367485_at	transcription elongation factor a (sii) 1	Up
1367495_at	similar to prefoldin 4	Up
1367503_at	similar to b-cell receptor-associated protein 31	Up
1367531_at	eukaryotic translation initiation factor 4h	Up
1367563_at	secreted acidic cysteine rich glycoprotein	Up
1367567_at	ribosomal protein l6	Up
1367568_a_at	matrix gla protein	Up
1367569_at, 1388244_s_at	laminin receptor 1 (ribosomal protein sa)	Up
1367570_at	transgelin	Up
1367573_at	ribosomal protein s6	Up
1367574_at	vimentin	Up
1367576_at	glutathione peroxidase 1	Up
1367579_a_at	tubulin, alpha 1	Up
1367579_a_at	tubulin, alpha 6	Up
1367579_a_at	similar to tubulin alpha-2 chain (alpha-tubulin 2)	Up
1367580_at	ribosomal protein l10a	Up
1367581_a_at	secreted phosphoprotein 1	Up
1367582_at	ribosomal protein l29	Up
1367584_at	annexin a2	Up
1367586_at	lactate dehydrogenase a	Up
1367590_at	ran, member ras oncogene family	Up
1367593_at	selenoprotein w, muscle 1	Up
1367596_at	ribosomal protein s26	Up
1367597_at	ribosomal protein s8	Up
1367600_at	desmin	Up
1367605_at	profilin 1	Up
1367614_at	annexin a1	Up
1367618_a_at	discs, large homolog 5 (drosophila) (predicted)	Up
1367628_at	lectin, galactose binding, soluble 1	Up
1367630_at	ribosomal protein s11	Up
1367631_at	connective tissue growth factor	Up
1367634_at	ribosomal protein l31	Up

Supplemental Data Table S8. Continued.

1367639_a_at	ribosomal protein s2	Up
1367640_at	ribosomal protein s12	Up
1367646_at	cathepsin b	Up
1367651_at	cathepsin d	Up
1367655_at	similar to thymosin, beta 10	Up
1367657_at	b-cell translocation gene 1, anti-proliferative	Up
1367663_at	protease (prosome, macropain) 28 subunit, alpha	Up
1367666_at	heterogeneous nuclear ribonucleoprotein h1	Up
1367671_at	proliferating cell nuclear antigen	Up
1367676_at	high mobility group box 2	Up
1367676_at	similar to high mobility group protein 2 (hmg-2)	Up
1367676_at	similar to high mobility group protein 2 (hmg-2)	Up
1367681_at	cd151 antigen	Up
1367690_at	signal sequence receptor 4	Up
1367691_at	protein kinase c, delta binding protein	Up
1367693_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	Up
1367701_at	receptor (calcitonin) activity modifying protein 2	Up
1367710_at	proteasome (prosome, macropain) 28 subunit, beta	Up
1367711_at	proteasome (prosome, macropain) 26s subunit, atpase 2	Up
1367712_at	tissue inhibitor of metalloproteinase 1	Up
1367713_at	eukaryotic translation initiation factor 2, subunit 1 alpha	Up
1367715_at	tumor necrosis factor receptor superfamily, member 1a	Up
1367721_at	syndecan 4	Up
1367722_at	dipeptidylpeptidase 7	Up
1367732_at, 1375705_at	guanine nucleotide binding protein, beta 1	Up
1367746_a_at	flotillin 2	Up
1367754_s_at	argininosuccinate lyase	Up
1367754_s_at, 1370309_a_at	heterogeneous nuclear ribonucleoprotein a/b	Up
1367765_at	transcobalamin 2	Up
1367768_at	latexin	Up
1367776_at	cell division cycle 2 homolog a (s. pombe)	Up
1367784_a_at	clusterin	Up
1367786_at	proteosome (prosome, macropain) subunit, beta type 8	Up
1367795_at	interferon-related developmental regulator 1	Up
1367800_at	plasminogen activator, tissue	Up
1367805_at	glutaminase	Up
1367816_at	homeobox only domain	Up
1367819_at	glutamate oxaloacetate transaminase 2	Up
1367820_at	barrier to autointegration factor 1	Up

Supplemental Data Table S8. Continued.

1367826_at	nuclear factor, erythroid derived 2, like 2	Up
1367833_at	peptidase (prosome, macropain) 26s subunit, atpase 5	Up
1367834_at	spermidine synthase	Up
1367844_at	guanine nucleotide binding protein, alpha inhibiting 2	Up
1367856_at	glucose-6-phosphate dehydrogenase	Up
1367857_at	fatty acid desaturase 1	Up
1367860_a_at	matrix metalloproteinase 14 (membrane-inserted)	Up
1367873_at	atpase, h+ transporting, lysosomal (vacuolar proton pump), subunit 1	Up
1367881_at	protein tyrosine phosphatase, non-receptor type substrate 1	Up
1367899_at	coagulation factor ii (thrombin) receptor	Up
1367900_at	glycogenin 1	Up
1367914_at	epithelial membrane protein 3	Up
1367925_at	major vault protein	Up
1367932_at	3-hydroxy-3-methylglutaryl-coenzyme a synthase 1	Up
1367942_at	acid phosphatase 5, tartrate resistant	Up
1367948_a_at	kinase insert domain protein receptor	Up
1367961_at	nerve growth factor, gamma	Up
1367974_at	annexin a3	Up
1367979_s_at	cytochrome p450, subfamily 51	Up
1367986_at	prostaglandin f2 receptor negative regulator	Up
1368000_at	complement component 3	Up
1368006_at	lysosomal-associated protein transmembrane 5	Up
1368036_at	protein tyrosine phosphatase, receptor type, f	Up
1368042_a_at	similar to high mobility group protein 1 (hmg-1) (amphoterin) (heparin-binding protein p30)	Up
1368042_a_at	similar to hmgb1 protein	Up
1368042_a_at	high mobility group box 1	Up
1368042_a_at	similar to high mobility group protein 1 (hmg-1) (amphoterin) (heparin-binding protein p30)	Up
1368052_at	tetraspanin 8	Up
1368055_a_at	lamin a	Up
1368065_at	regulator of g-protein signaling 19 interacting protein 1	Up
1368073_at	interferon regulatory factor 1	Up
1368083_at	cyclin h	Up
1368102_at	hydroxysteroid 11-beta dehydrogenase 2	Up
1368143_at	annexin a7	Up
1368146_at	dual specificity phosphatase 1	Up
1368160_at	insulin-like growth factor binding protein 1	Up
1368168_at	solute carrier family 34 (sodium phosphate), member 2	Up
1368173_at	nucleolar protein 5	Up
1368187_at	glycoprotein (transmembrane) nmb	Up

Supplemental Data Table S8. Continued.

1368199_at	nucleoporin 88	Up
1368204_at	ligase i, dna, atp-dependent	Up
1368204_at	ligase i, dna, atp-dependent (predicted)	Up
1368223_at	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 1	Up
1368224_at	serine protease inhibitor	Up
1368280_at, 1374778_at	cathepsin c	Up
1368290_at	cysteine rich protein 61	Up
1368308_at	myelocytomatosis viral oncogene homolog (avian)	Up
1368321_at	early growth response 1	Up
1368322_at	superoxide dismutase 3, extracellular	Up
1368331_at	chitobiase, di-n-acetyl-	Up
1368356_a_at, 1399161_a_at	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator	Up
1368361_a_at	protein tyrosine phosphatase, non-receptor type 2	Up
1368368_a_at	liver-specific bhlh-zip transcription factor 7	Up
1368395_at	glypican 3	Up
1368412_a_at	protein tyrosine phosphatase, receptor type, o	Up
1368420_at	ceruloplasmin	Up
1368430_at	legumain	Up
1368471_at	guanylate cyclase activator 2a	Up
1368474_at	vascular cell adhesion molecule 1	Up
1368490_at	cd14 antigen	Up
1368589_at	protein tyrosine phosphatase, receptor type, j	Up
1368702_at	prkc, apoptosis, wt1, regulator	Up
1368727_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 9	Up
1368732_at	transporter 2, atp-binding cassette, sub-family b (mdr/tap)	Up
1368762_at	ubiquitin d	Up
1368790_at	serine (or cysteine) proteinase inhibitor, clade a (alpha-1 antiproteinase, antitrypsin), member 10	Up
1368808_at, 1368809_at	cap, adenylate cyclase-associated protein 1 (yeast)	Up
1368817_at	proteasome (prosome, macropain) activator subunit 4	Up
1368819_at, 1387346_at	integrin beta 1 (fibronectin receptor beta)	Up
1368826_at	catechol-o-methyltransferase	Up
1368834_at	calcium/calmodulin-dependent protein kinase ii, delta	Up
1368838_at, 1371653_at	tropomyosin 4	Up
1368840_at	lr8 protein	Up
1368862_at, 1383126_at	thymoma viral proto-oncogene 1	Up

Supplemental Data Table S8. Continued.

1368869_at	a kinase (prka) anchor protein (gravin) 12	Up
1368871_at	mitogen activated protein kinase kinase kinase 1	Up
1368878_at	isopentenyl-diphosphate delta isomerase	Up
1368888_a_at	reticulon 4	Up
1368921_a_at, 1387952_a_at, 1390659_at	cd44 antigen	Up
1368967_at	eukaryotic translation initiation factor 2b, subunit 3 gamma	Up
1369008_a_at	olfactomedin 1	Up
1369013_a_at	mitochondrial ribosomal protein l17	Up
1369029_at	phospholipid scramblase 1	Up
1369319_at, 1374387_at	adp-ribosylation factor-like 6 interacting protein 5	Up
1369665_a_at	interleukin 18	Up
1369712_at	serine/threonine kinase 3 (ste20 homolog, yeast)	Up
1369736_at, 1371527_at	epithelial membrane protein 1	Up
1369814_at	chemokine (c-c motif) ligand 20	Up
1369895_s_at	podocalyxin-like	Up
1369930_at	proteasome (prosome, macropain) subunit, alpha type 6	Up
1369934_at	peptidylprolyl isomerase b	Up
1369936_at, 1372770_at, 1369937_at, 1370246_at	calmodulin 1	Up
1369941_at	death-associated protein	Up
1369943_at	transglutaminase 2, c polypeptide	Up
1369944_at	marcks-like protein	Up
1369950_at	cyclin-dependent kinase 4	Up
1369952_at	poly(a) binding protein, cytoplasmic 1	Up
1369953_a_at	cd24 antigen	Up
1369956_at	interferon gamma receptor 1	Up
1369958_at	rhob gene	Up
1369962_at	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/imp cyclohydrolase	Up
1369964_at	coronin, actin binding protein 1a	Up
1369966_a_at	ribosomal protein s24	Up
1369969_at	adp-ribosyltransferase 1	Up
1369976_at	dynein, cytoplasmic, light chain 1	Up
1369991_at	signal peptidase complex 18kd	Up
1369996_at	polymerase (rna) ii (dna directed) polypeptide f	Up
1369998_at, 1376268_at	adp-ribosylation factor 6	Up
1370014_at	syntaxin 4a (placental)	Up

Supplemental Data Table S8. Continued.

1370050_at	atpase, ca++ transporting, plasma membrane 1	Up
1370057_at	cysteine and glycine-rich protein 1	Up
1370062_at	hypoxia induced gene 1	Up
1370073_at	protein kinase inhibitor p58	Up
1370086_at	fibrinogen, gamma polypeptide	Up
1370154_at	lysozyme	Up
1370155_at	procollagen, type i, alpha 2	Up
1370156_at	prion protein	Up
1370161_at	steroid sensitive gene 1	Up
1370168_at, 1387862_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide	Up
1370170_at	heterogeneous nuclear ribonucleoprotein u	Up
1370184_at	cofilin 1	Up
1370186_at	proteosome (prosome, macropain) subunit, beta type 9	Up
1370188_at, 1370189_at	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, drosophila)	Up
1370204_at	fgf receptor activating protein 1	Up
1370215_at	complement component 1, q subcomponent, beta polypeptide	Up
1370224_at, 1371781_at	signal transducer and activator of transcription 3	Up
1370234_at	fibronectin 1	Up
1370242_at	ribosomal protein s23	Up
1370244_at, 1370245_at	cathepsin l	Up
1370249_at	benzodiazepine receptor, peripheral	Up
1370250_at	ubiquitin-conjugating enzyme e2i	Up
1370250_at	similar to riken cdna a930001m12 gene	Up
1370253_at	ribosomal protein l22	Up
1370258_at	basic leucine zipper and w2 domains 2	Up
1370262_at	metadherin	Up
1370280_at	hypoxanthine guanine phosphoribosyl transferase	Up
1370287_a_at, 1370288_a_at	tropomyosin 1, alpha	Up
1370290_at, 1387892_at	tubulin, beta 5	Up
1370294_a_at	cell division cycle 20 homolog (s. cerevisiae)	Up
1370307_at	agrin	Up
1370308_at	rs21-c6 protein	Up
1370314_at	solute carrier family 20 (phosphate transporter), member 1	Up
1370339_at, 1371239_s_at, 1398303_s_at, 1370340_x_at	tropomyosin 3, gamma	Up
1370346_at	cyclin b1	Up

Supplemental Data Table S8. Continued.

1370347_at	pdz and lim domain 7	Up
1370376_a_at	cold shock domain protein a	Up
1370401_at	lymphocyte antigen 6 complex, locus b	Up
1370462_at	hyaluronan mediated motility receptor	Up
1370467_at, 1370468_at	solute carrier family 13, member 1	Up
1370511_at	fibrinogen, b beta polypeptide	Up
1370554_at	ubiquitin carboxyl-terminal esterase l3 (ubiquitin thiolesterase)	Up
1370554_at	similar to ubiqutin carboxyl-terminal hydrolase l3	Up
1370807_at	vacuole membrane protein 1	Up
1370826_at, 1371872_at	nucleosome assembly protein 1-like 1	Up
1370845_at	ectonucleoside triphosphate diphosphohydrolase 2	Up
1370855_at	cystatin c	Up
1370859_at	protein disulfide isomerase associated 6	Up
1370871_at	hypothetical gene supported by y16641; y16641	Up
1370887_at	transforming growth factor beta 1 induced transcript 1	Up
1370890_at	arp3 actin-related protein 3 homolog (yeast)	Up
1370892_at	complement component 4a	Up
1370892_at	complement component 4, gene 2	Up
1370894_at	claudin 7	Up
1370904_at	major histocompatibility complex, class ii, dm alpha	Up
1370910_at	replication factor c (activator 1) 2	Up
1370928_at	lps-induced tn factor	Up
1370968_at	nuclear factor of kappa light chain gene enhancer in b-cells 1, p105	Up
1370976_at	ras-gtpase-activating protein sh3-domain binding protein	Up
1370992_a_at, 1371258_at	fibrinogen, alpha polypeptide	Up
1371021_at, 1375412_at	arylsulfatase b	Up
1371099_at	polymeric immunoglobulin receptor	Up
1371237_a_at, 1388271_at	metallothionein 1a	Up
1371244_at	adenine phosphoribosyl transferase (predicted)	Up
1371246_at	nuclear transport factor 2	Up
1371295_at	ribosomal protein s20	Up
1371299_at	ribosomal protein s3	Up
1371300_at	ribosomal protein l3	Up
1371305_at	ribosomal protein l8	Up
1371308_at	ribosomal protein s4, x-linked	Up
1371310_s_at	serine (or cysteine) proteinase inhibitor, clade h, member 1	Up
1371318_at	ribosomal protein s16	Up
1371330_at	ribosomal protein l11	Up

Supplemental Data Table S8. Continued.

1371331_at	follistatin-like 1	Up
1371336_at, 1388581_at	hematological and neurological expressed sequence 1	Up
1371341_at	small nuclear ribonucleoprotein d2 (predicted)	Up
1371344_at	ribosomal protein l27a (predicted)	Up
1371352_at	high mobility group nucleosomal binding domain 2	Up
1371365_at	similar to ubiquitin-conjugating enzyme e2s	Up
1371366_at	rho gdp dissociation inhibitor (gdi) alpha	Up
1371377_at	ribosomal protein s19	Up
1371382_at	similar to filamin a (alpha-filamin) (filamin 1) (endothelial actin-binding protein) (actin-binding protein 280) (abp-280) (nonmuscle filamin)	Up
1371390_at	tubulin, beta, 2	Up
1371391_at	thioredoxin domain containing 5 (predicted)	Up
1371395_at	chromobox homolog 3 (hp1 gamma homolog, drosophila)	Up
1371402_at, 1387664_at	atpase, h+ transporting, v1 subunit b, isoform 2	Up
1371410_at	similar to cdna sequence bc056474	Up
1371422_at	morf-related gene x	Up
1371432_at	vesicle amine transport protein 1 homolog (t californica)	Up
1371440_at	beta-2 microglobulin	Up
1371441_at	phosphoprotein enriched in astrocytes 15	Up
1371447_at	placenta-specific 8 (predicted)	Up
1371465_at	cortactin isoform b	Up
1371469_at	calcium binding protein p22	Up
1371474_at	mitochondrial carrier homolog 1 (c. elegans)	Up
1371487_at	sh3 domain binding glutamic acid-rich protein-like 3 (predicted)	Up
1371495_at	cation-dependent mannose-6-phosphate receptor	Up
1371509_at	transforming growth factor beta regulated gene 1	Up
1371511_at	actin related protein 2/3 complex, subunit 2 (predicted)	Up
1371530_at	keratin complex 2, basic, gene 8	Up
1371533_at	dynactin 6 (predicted)	Up
1371539_at	nucleolar protein family a, member 2 (predicted)	Up
1371544_at	similar to enhancer of rudimentary homolog	Up
1371573_at	large subunit ribosomal protein l36a	Up
1371583_at	rna binding motif protein 3	Up
1371596_at	ribonucleic acid binding protein s1	Up
1371622_at	similar to candidate tumor suppressor ovca2	Up
1371632_at	selectin, platelet (p-selectin) ligand (predicted)	Up
1371644_at	protein tyrosine kinase 9	Up
1371648_at, 1399162_a_at	damage-specific dna binding protein 1	Up
1371656_at	chaperonin subunit 4 (delta)	Up

Supplemental Data Table S8. Continued.

1371657_at	ubiquitin-like 1 (sentrin) activating enzyme e1b	Up
1371662_at	lysyl-trna synthetase	Up
1371676_at	longevity assurance homolog 5 (s. cerevisiae) (predicted)	Up
1371691_at	retinoic acid receptor responder (tazarotene induced) 2	Up
1371724_at	small fragment nuclease	Up
1371725_at, 1387402_at	myosin, heavy polypeptide 9	Up
1371774_at	spermidine/spermine n1-acetyl transferase (mapped)	Up
1371776_at	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1	Up
1371782_at	nipsnap-related protein	Up
1371785_at	tumor necrosis factor receptor superfamily, member 12a	Up
1371786_at	tripartite motif-containing 35	Up
1371790_at	mitochondrial ribosomal protein l45 (predicted)	Up
1371830_at	ubiquitin-like 1 (sentrin) activating enzyme e1a	Up
1371838_at	similar to splicing factor, arginine/serine-rich 2	Up
1371856_at	proline-rich nuclear receptor coactivator 2	Up
1371871_at	rab12, member ras oncogene family	Up
1371887_at	similar to high mobility group protein homolog hmg4	Up
1371888_at	mitochondrial ribosomal protein l24	Up
1371918_at	cd99 antigen	Up
1371926_at, 1373140_at	interleukin 6 signal transducer	Up
1371936_at	eukaryotic translation initiation factor 4a1	Up
1371938_at, 1371939_at	gpi-anchored membrane protein 1	Up
1371969_at	caldesmon 1	Up
1371970_at	similar to expressed sequence aw413625	Up
1371977_at	actin related protein 2/3 complex, subunit 3 (predicted)	Up
1371978_at	oxysterol binding protein-like 9 (predicted)	Up
1371985_a_at	hla-b associated transcript 5	Up
1371989_at	high mobility group nucleosomal binding domain 3	Up
1372004_at	heme binding protein 1 (predicted)	Up
1372009_at	tyrosyl-trna synthetase	Up
1372013_at	interferon induced transmembrane protein 1 (predicted)	Up
1372043_at	similar to ribosomal protein p0-like protein; 60s acidic ribosomal protein po; ribosomal protein, large, p0-like (predicted)	Up
1372056_at	chemokine-like factor super family 6	Up
1372064_at	similar to chemokine (c-x-c motif) ligand 16	Up
1372071_at	similar to 8d6 antigen	Up
1372082_at	unknown (protein for mgc:72598)	Up
1372090_at	similar to riken cdna 1700108m19	Up
1372094_at	suppressor of ty 5 homolog (s. cerevisiae)	Up
1372108_at	similar to riken cdna 2810422b04	Up

Supplemental Data Table S8. Continued.

1372155_at	tripartite motif protein 28	Up
1372181_at	replication protein a1	Up
1372219_at	similar to tropomyosin 1, embryonic fibroblast - rat	Up
1372241_at	ornithine decarboxylase antizyme 1	Up
1372246_at	osteoclast stimulating factor 1	Up
1372255_at	arginyl-trna synthetase (predicted)	Up
1372256_at	,gb:bf550246 /db_xref=gi:11659934 /db_xref=ui-r-e0-cx-g-02-0-ui.r1 /clone=ui-r-e0-cx-g-02-0-ui /fea=est /cnt=18 /tid=rn.8405.1 /tier=stack /stk=12 /ug=rn.8405 /ug_title=ests, highly similar to cysteine-rich intestinal protein (r.norvegicus)	Up
1372267_at	proteasome (prosome, macropain) 26s subunit, non-atpase, 5 (predicted)	Up
1372269_at	mediator of rna polymerase ii transcription, subunit 6 homolog (yeast) (predicted)	Up
1372293_at	toll-like receptor 5	Up
1372333_at	similar to small nuclear ribonucleoprotein e	Up
1372333_at	small nuclear ribonucleoprotein e (predicted)	Up
1372352_at	arginine-rich, mutated in early stage tumors (predicted)	Up
1372369_at	similar to mitsugumin 23	Up
1372389_at	immediate early response 2	Up
1372399_at	similar to cofactor of brca1; negative elongation factor protein b (predicted)	Up
1372401_at	n-acetylneuraminic acid synthase (sialic acid synthase) (predicted)	Up
1372404_at	ras-related c3 botulinum substrate 2	Up
1372406_at	similar to dna replication licensing factor mcm3 (dna polymerase alpha holoenzyme-associated protein p1) (p1-mcm3)	Up
1372406_at	minichromosome maintenance deficient 3 (s. cerevisiae) (predicted)	Up
1372420_at	similar to fksg24 (predicted)	Up
1372433_at	similar to cg11030-pa (predicted)	Up
1372439_at, 1373245_at	procollagen, type iv, alpha 1	Up
1372459_at	vasodilator-stimulated phosphoprotein (predicted)	Up
1372461_at	loc499767	Up
1372461_at	set translocation (predicted)	Up
1372473_at	tight junction protein 1 (predicted)	Up
1372500_at	tropomodulin 3	Up
1372501_at	splicing factor 3b, subunit 3 (predicted)	Up
1372513_at	ras-related c3 botulinum toxin substrate 1 (rho family, small gtp binding protein rac1)	Up
1372516_at	kinesin family member 22	Up
1372520_at	myeloid cell leukemia sequence 1	Up
1372543_at	similar to riken cdna 2610029g23	Up
1372564_at	v-ets erythroblastosis virus e26 oncogene homolog 2 (avian) (mapped)	Up

Supplemental Data Table S8. Continued.

1372571_at	similar to 9530046h09rik protein	Up
1372577_at	actin related protein 2/3 complex, subunit 4 (predicted)	Up
1372607_at	nucleotide binding protein 2	Up
1372620_at	acidic (leucine-rich) nuclear phosphoprotein 32 family, member e	Up
1372634_at	adp-ribosylhydrolase like 2 (predicted)	Up
1372667_at	similar to riken cdna 1110059e24	Up
1372685_at	cyclin-dependent kinase inhibitor 3 (predicted)	Up
1372691_at	uridine phosphorylase 1	Up
1372697_at	mitochondrial ribosomal protein s15	Up
1372707_at	rab6a, member ras oncogene family	Up
1372709_at	b-cell receptor-associated protein bap29	Up
1372739_at	sarcoma amplified sequence	Up
1372752_at	transmembrane 4 superfamily member 7	Up
1372755_at	mal, t-cell differentiation protein 2	Up
1372773_at	neural proliferation, differentiation and control, 1	Up
1372778_at	solute carrier family 39 (zinc transporter), member 1 (predicted)	Up
1372787_at	charged amino acid rich leucine zipper 1	Up
1372815_at	mago-nashi homolog, proliferation-associated (drosophila) (predicted)	Up
1372886_at	transforming acidic coiled coil 3	Up
1372914_at	lymphotoxin b receptor	Up
1372919_at	similar to putative lysophosphatidic acid acyltransferase	Up
1372990_at	camp responsive element binding protein 3	Up
1373025_at	complement component 1, q subcomponent, gamma polypeptide	Up
1373030_at	loc501594	Up
1373035_at	similar to cdna sequence bc017158	Up
1373040_at	eukaryotic translation initiation factor 3, subunit 5 (epsilon) (predicted)	Up
1373047_at	protein kinase c, lambda	Up
1373054_at	cdw92 antigen	Up
1373072_at	,gb:ai170552 /db_xref=gi:3710592 /db_xref=est216483 /clone=rlucq61 /fea=est /cnt=14 /tid=rn.1897.1 /tier=stack /stk=9 /ug=rn.1897 /ug_title=ests	Up
1373087_at	axotrophin	Up
1373116_at	karyopherin (importin) alpha 3	Up
1373130_at	myomesin 2	Up
1373152_at	protease, serine, 23	Up
1373164_at	serine/threonine kinase 17b (apoptosis-inducing)	Up
1373204_at	hypothetical loc297077	Up
1373209_at	,gb:ai599284 /db_xref=gi:4608332 /db_xref=est250987 /clone=remeq46 /fea=est /cnt=12 /tid=rn.16374.1 /tier=stack /stk=9 /ug=rn.16374 /ug_title=ests	Up
1373250_at	similar to 60s ribosomal protein l7a	Up

Supplemental Data Table S8. Continued.

1373385_at	similar to mahogunin, ring finger 1; mahoganoid	Up
1373387_at	similar to hypothetical protein dc50 (predicted)	Up
1373392_at	tpa regulated locus	Up
1373393_at	similar to ext1	Up
1373397_at, 1375525_at	microtubule-associated protein, rp/eb family, member 1	Up
1373399_at	wd repeat domain 6	Up
1373403_at	,gb:ai230625 /db_xref=gi:3814512 /db_xref=est227320 /clone=remcz18 /fea=est /cnt=14 /tid=rn.24073.1 /tier=stack /stk=8 /ug=rn.24073 /ug_title=ests	Up
1373419_at	protein tyrosine phosphatase, receptor type, g	Up
1373421_at	tg interacting factor	Up
1373447_at	similar to hn1-like protein	Up
1373488_at	,gb:bf289154 /db_xref=gi:11220224 /db_xref=est453745 /clone=rgihb70 /fea=est /cnt=11 /tid=rn.41269.1 /tier=stack /stk=8 /ug=rn.41269 /ug_title=ests	Up
1373575_at	similar to nadh dehydrogenase (ubiquinone) fe-s protein 2	Up
1373592_at	similar to spi6	Up
1373595_at	similar to riken cdna 1200015a22	Up
1373650_at	cytidine monophospho-n-acetylneuraminic acid synthetase	Up
1373658_at	rac gtpase-activating protein 1 (predicted)	Up
1373682_at	dead (asp-glu-ala-asp) box polypeptide 51 (predicted)	Up
1373718_at	similar to tubulin, beta 2	Up
1373780_at	tetraspan 1	Up
1373822_at	similar to riken cdna 1110025l05	Up
1373823_at	similar to cyclin-dependent kinases regulatory subunit 2 (cks-2)	Up
1373848_at	similar to riken cdna 5730449l18 (predicted)	Up
1373849_at	similar to baf53a	Up
1373877_at	phosphatidylinositol binding clathrin assembly protein	Up
1373897_at	lamin b1	Up
1373900_at	keratin complex 2, basic, gene 7 (predicted)	Up
1373908_at	,gb:ai407002 /db_xref=gi:4250506 /db_xref=est235290 /clone=rovdv15 /fea=est /cnt=12 /tid=rn.41951.1 /tier=stack /stk=7 /ug=rn.41951 /ug_title=ests	Up
1373951_at	protein kinase, camp dependent regulatory, type i, alpha	Up
1373983_at	loc360807	Up
1374015_at	,gb:bf281697 /db_xref=gi:11212767 /db_xref=est446288 /clone=rgiap26 /fea=est /cnt=9 /tid=rn.7770.1 /tier=stack /stk=7 /ug=rn.7770 /ug_title=ests	Up
1374033_at	proteasome (prosome, macropain) subunit, beta type 10	Up
1374036_at	minichromosome maintenance deficient 2 mitotin (s. cerevisiae) (predicted)	Up

Supplemental Data Table S8. Continued.

1374065_at	,gb:bg378920 /db_xref=gi:13303392 /db_xref=ui-r-cv1-bvu-e-07-0-ui.s1 /clone=ui-r-cv1-bvu-e-07-0-ui /fea=est /cnt=13 /tid=rn.38245.1 /tier=stack /stk=7 /ug=rn.38245 /ug_title=ests	Up
1374069_at, 1398814_at	rab11a, member ras oncogene family	Up
1374070_at	glutathione peroxidase 2	Up
1374163_at	anaphase promoting complex subunit 4	Up
1374180_at	eukaryotic translation initiation factor 1a	Up
1374228_at	tripartite motif protein 47 (predicted)	Up
1374276_at	similar to spt3-associated factor 42	Up
1374292_at	similar to riken cdna 1110031i02	Up
1374388_at	ef hand domain containing 2	Up
1374397_at	eukaryotic translation initiation factor 2, subunit 2 (beta)	Up
1374406_at	kelch domain containing 2	Up
1374449_at	similar to cell division cycle associated 3	Up
1374449_at	cell division cycle associated 3	Up
1374456_at	,gb:ai179562 /db_xref=gi:3730200 /db_xref=est223283 /clone=rspci95 /fea=est /cnt=11 /tid=rn.4141.1 /tier=stack /stk=6 /ug=rn.4141 /ug_title=ests	Up
1374457_at	similar to serine c-palmitoyltransferase	Up
1374468_at	myeloid differentiation primary response gene 88	Up
1374499_at	tata box binding protein (tbp)-associated factor, rna polymerase i, a	Up
1374501_at	similar to rna-binding protein isoform g3bp-2a	Up
1374515_at	similar to riken cdna 6330409n04	Up
1374630_at	chloride intracellular channel 3	Up
1374678_at	sema domain, immunoglobulin domain (ig), transmembrane domain (tm) and short cytoplasmic domain, (semaphorin) 4b	Up
1374700_at	sprouty protein with evh-1 domain 1, related sequence	Up
1374718_at	similar to deltex 3-like	Up
1374730_at	tyro protein tyrosine kinase binding protein	Up
1374775_at	antigen identified by monoclonal antibody ki-67 (predicted)	Up
1374775_at	similar to ki-67	Up
1374775_at	similar to mki67 protein	Up
1374806_at	stratifin (predicted)	Up
1374840_at	,gb:bg377716 /db_xref=gi:13302188 /db_xref=ui-r-cu0-bva-b-11-0-ui.s1 /clone=ui-r-cu0-bva-b-11-0-ui /fea=est /cnt=7 /tid=rn.41174.1 /tier=stack /stk=6 /ug=rn.41174 /ug_title=ests, weakly similar to cypb rat peptidyl-prolyl cis-trans isomerase b precursor (r.norvegicus)	Up
1374857_at	similar to nucleolar protein family a, member 1	Up
1374876_at	leptin receptor overlapping transcript-like 1	Up
1374897_at	tho complex 4 (predicted)	Up

Supplemental Data Table S8. Continued.

1374927_at	,gb:ai714124 /db_xref=gi:5017924 /db_xref=ui-r-af1-aaq-g-09-0-ui.s1 /clone=ui-r-af1-aaq-g-09-0-ui /fea=est /cnt=7 /tid=rn.14945.1 /tier=stack /stk=6 /ug=rn.14945 /ug_title=ests	Up
1375003_at	serine (or cysteine) peptidase inhibitor, clade b, member 6	Up
1375034_at	lysosomal phospholipase a2	Up
1375043_at	fbj murine osteosarcoma viral oncogene homolog	Up
1375161_at	mitochondrial ribosomal protein l55 (predicted)	Up
1375170_at	s100 calcium binding protein a11 (calizzarin) (predicted)	Up
1375181_at	similar to 60s ribosomal protein l12	Up
1375211_at	ribonuclease t2 (predicted)	Up
1375213_at	phosphoenolpyruvate carboxykinase 2 (mitochondrial) (predicted)	Up
1375216_at	poliovirus receptor-related 2 (herpesvirus entry mediator b)	Up
1375230_at	,gb:aa800192 /db_xref=gi:2863147 /db_xref=est189689 /clone=rheam29 /fea=est /cnt=16 /tid=rn.8571.1 /tier=stack /stk=13 /ug=rn.8571 /ug_title=ests	Up
1375266_at	cyclin d2	Up
1375362_at	similar to riken cdna 2010106g01	Up
1375530_at	similar to emeg32 protein	Up
1375538_at	vinculin (predicted)	Up
1375550_at	bcl2-associated athanogene 1 (predicted)	Up
1375559_at	,gb:bi283479 /db_xref=gi:14935262 /db_xref=ui-r-de0-cab-g-09-0-ui.s1 /clone=ui-r-de0-cab-g-09-0-ui /fea=est /cnt=9 /tid=rn.40945.1 /tier=stack /stk=7 /ug=rn.40945 /ug_title=ests, weakly similar to lhx5 mouse limhomeobox protein lhx5 (r.norvegicus)	Up
1375612_at, 1387872_at	heterogeneous nuclear ribonucleoprotein a1	Up
1375653_at	neurexin 3	Up
1375654_at	cytoskeleton-associated protein 4 (predicted)	Up
1375686_at	peptidylprolyl isomerase (cyclophilin)-like 3	Up
1375706_at	,gb:ai230273 /db_xref=gi:3814160 /db_xref=est226968 /clone=remcu45 /fea=est /cnt=8 /tid=rn.16503.1 /tier=stack /stk=6 /ug=rn.16503 /ug_title=ests	Up
1375848_at	paraoxonase 2	Up
1375854_at	similar to beta-catenin-interacting protein icat	Up
1375857_at	similar to myoferlin (fer-1 like protein 3)	Up
1375895_at	serine racemase	Up
1375913_at	udp-n-acetyl-alpha-d-galactosamine:polypeptide n-acetylgalactosaminyltransferase 2 (predicted)	Up
1375928_at	similar to histone-lysine n-methyltransferase, h4 lysine-20 specific (histone h4-k20 methyltransferase) (h4-k20-hmtase) (set domain-containing protein 8) (pr/set domain-containing protein 07) (pr/set07) (pr-set7) (predicted)	Up
1375928_at	similar to set domain-containing protein	Up
1375989_a_at	similar to nuclear factor kappa b subunit p100	Up
1376029_at	rab2, member ras oncogene family-like	Up

Supplemental Data Table S8. Continued.

1376055_at	,gb:aa859768 /db_xref=gi:4230309 /db_xref=ui-r-e0-bx-d-12-0-ui.s1 /clone=ui-r-e0-bx-d-12-0-ui /fea=est /cnt=7 /tid=rn.123.1 /tier=consend /stk=5 /ug=rn.123 /ug_title=ests	Up
1376089_at	low density lipoprotein receptor	Up
1376102_at	similar to recs1	Up
1376109_at	,gb:bm387711 /db_xref=gi:18187764 /db_xref=ui-r-cn1-cjj-j-06-0-ui.s1 /clone=ui-r-cn1-cjj-j-06-0-ui /fea=est /cnt=6 /tid=rn.48053.1 /tier=consend /stk=5 /ug=rn.48053 /ug_title=ests	Up
1376129_at	similar to vacuolar protein sorting 13c protein	Up
1376144_at	similar to b aggressive lymphoma (predicted)	Up
1376151_a_at	interferon gamma induced gtpase	Up
1376153_at	,gb:be102621 /db_xref=gi:8494720 /db_xref=ui-r-bt1-aqs-b-05-0-ui.s1 /clone=ui-r-bt1-aqs-b-05-0-ui /fea=est /cnt=6 /tid=rn.22233.1 /tier=consend /stk=5 /ug=rn.22233 /ug_title=ests	Up
1376199_at	cell cycle related kinase	Up
1376570_at	chaperonin subunit 5 (epsilon)	Up
1376641_at	tho complex 1	Up
1376687_at	ubiquitin specific protease 1	Up
1376700_at	,gb:ai179472 /db_xref=gi:3730110 /db_xref=est223186 /clone=rspch80 /fea=est /cnt=7 /tid=rn.43951.1 /tier=consend /stk=4 /ug=rn.43951 /ug_title=ests	Up
1376706_at	,gb:bg373822 /db_xref=gi:13270359 /db_xref=ui-r-cv1-bsk-c-11-0-ui.s1 /clone=ui-r-cv1-bsk-c-11-0-ui /fea=est /cnt=7 /tid=rn.16447.1 /tier=consend /stk=4 /ug=rn.16447 /ug_title=ests	Up
1376722_at	nucleoporin 205kda (predicted)	Up
1376835_at	solute carrier family 35, member b2	Up
1376976_at	secreted and transmembrane 1	Up
1377092_at	,gb:bf389682 /db_xref=gi:11374517 /db_xref=ui-r-bs2-bdn-e-06-0-ui.s1 /clone=ui-r-bs2-bdn-e-06-0-ui /fea=est /cnt=5 /tid=rn.41848.1 /tier=consend /stk=4 /ug=rn.41848 /ug_title=ests	Up
1377103_at	,gb:aw525765 /db_xref=gi:7168150 /db_xref=ui-r-bj0p-air-e-10-0-ui.s1 /clone=ui-r-bj0p-air-e-10-0-ui /fea=est /cnt=5 /tid=rn.19310.1 /tier=consend /stk=4 /ug=rn.19310 /ug_title=ests	Up
1377194_a_at	similar to riken cdna 2310015n07	Up
1377299_at	nuclear autoantigenic sperm protein	Up
1377379_at	interferon regulatory factor 6 (predicted)	Up
1379497_at	,gb:bi275261 /db_xref=gi:14886936 /db_xref=ui-r-cx0-bwr-d-11-0-ui.s1 /clone=ui-r-cx0-bwr-d-11-0-ui /fea=est /cnt=5 /tid=rn.24928.1 /tier=consend /stk=2 /ug=rn.24928 /ug_title=ests	Up
1382778_at	dual specificity phosphatase 6	Up
1383175_a_at, 1392938_s_at, 1385458_a_at	similar to c11orf17 protein (predicted)	Up
1383222_at	ferm-domain-containing protein 163scii	Up

Supplemental Data Table S8. Continued.

1383349_at	,gb:be115594 /db_xref=gi:8507699 /db_xref=ui-r-bj1-avw-g-01-0-ui.s1 /clone=ui-r-bj1-avw-g-01-0-ui /fea=est /cnt=6 /tid=rn.19941.1 /tier=consend /stk=0 /ug=rn.19941 /ug_title=ests	Up
1383855_at	similar to riken cdna 2210008a03 gene	Up
1383912_at	headcase homolog (drosophila) (predicted)	Up
1384548_at	ribosomal protein l32	Up
1386858_at, 1398872_at	ribosomal protein l13	Up
1386861_at	h2a histone family, member z	Up
1386862_at	annexin a5	Up
1386863_at	protein phosphatase 1, catalytic subunit, alpha isoform	Up
1386879_at	lectin, galactose binding, soluble 3	Up
1386882_at	t-complex testis expressed 1	Up
1386890_at	s100 calcium binding protein a10 (calpactin)	Up
1386893_at	granulin	Up
1386897_at	heterogeneous nuclear ribonucleoproteins methyltransferase-like 2 (s. cerevisiae)	Up
1386907_at	enolase 3, beta	Up
1386910_a_at	apurinic/apyrimidinic endonuclease 1	Up
1386912_at	procollagen c-proteinase enhancer protein	Up
1386913_at	glycoprotein 38	Up
1386921_at	carboxypeptidase e	Up
1386925_at	actin related protein 2/3 complex, subunit 1b	Up
1386940_at	tissue inhibitor of metalloproteinase 2	Up
1386941_at	plectin 1	Up
1386976_at	kangai 1	Up
1386994_at, 1386995_at	b-cell translocation gene 2, anti-proliferative	Up
1387005_at	cathepsin s	Up
1387015_at	profilin 2	Up
1387017_at	squalene epoxidase	Up
1387039_at	glypican 1	Up
1387040_at	myelin and lymphocyte protein	Up
1387048_at	nuclear rna helicase, decd variant of dead box family	Up
1387050_s_at	similar to alpha-1 major acute phase protein prepeptide	Up
1387050_s_at	kininogen 1	Up
1387060_at, 1388986_at	core promoter element binding protein	Up
1387076_at	hypoxia inducible factor 1, alpha subunit	Up
1387101_at	acyl-coa synthetase long-chain family member 4	Up
1387130_at	solute carrier family 39 (iron-regulated transporter), member 1	Up
1387144_at	integrin alpha 1	Up
1387188_at	solute carrier family 17 (sodium phosphate), member 1	Up

Supplemental Data Table S8. Continued.

1387202_at	intercellular adhesion molecule 1	Up
1387219_at	adrenomedullin	Up
1387228_at	solute carrier family 2 (facilitated glucose transporter), member 2	Up
1387279_at	junctional adhesion molecule 1	Up
1387343_at	ccaat/enhancer binding protein (c/ebp), delta	Up
1387659_at	guanine deaminase	Up
1387770_at	putative isg12(a) protein	Up
1387774_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	Up
1387798_a_at	complement receptor related protein	Up
1387806_at	ras related protein 1b	Up
1387808_at	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	Up
1387820_at	kallikrein 7	Up
1387868_at	lipopolysaccharide binding protein	Up
1387883_a_at	thymosin, beta 4	Up
1387888_at	ribosomal protein s9	Up
1387891_at	peroxiredoxin 4	Up
1387925_at	asparagine synthetase	Up
1387965_at	kidney injury molecule 1	Up
1387969_at	chemokine (c-x-c motif) ligand 10	Up
1387995_a_at	interferon-inducible protein variant 10	Up
1388107_at	protein phosphatase 2, regulatory subunit b, delta isoform	Up
1388114_at	myosin light chain, regulatory b	Up
1388116_at	collagen, type 1, alpha 1	Up
1388119_at	similar to hnrpa3 protein	Up
1388119_at	heterogeneous nuclear ribonucleoprotein a3	Up
1388119_at	similar to hnrpa3 protein	Up
1388119_at	hypothetical gene supported by y16641	Up
1388126_at	multiple inositol polyphosphate histidine phosphatase 1	Up
1388131_at	similar to tubulin, beta	Up
1388134_at	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	Up
1388150_at	exportin 1, crm1 homolog (yeast)	Up
1388158_at	hla-b-associated transcript 1a	Up
1388182_at	dna primase, p49 subunit	Up
1388297_at	eukaryotic translation elongation factor 1 gamma	Up
1388314_at	high mobility group nucleosomal binding domain 1	Up
1388328_at	similar to eukaryotic translation initiation factor 3 subunit 2 (eif-3 beta) (eif3 p36) (eif3i) (tgf-beta receptor interacting protein 1) (trip-1)	Up
1388335_at	transgelin 2	Up
1388337_at	nucleoside phosphorylase (mapped)	Up
1388340_at	ns5a (hepatitis c virus) transactivated protein 9	Up

Supplemental Data Table S8. Continued.

1388353_at	proliferation-associated 2g4	Up
1388354_at	similar to u5 snrnp-specific protein, 200 kda	Up
1388356_at	s100 calcium binding protein a16 (predicted)	Up
1388388_at	protein phosphatase 2, regulatory subunit b (b56), delta isoform	Up
1388389_at	septin 2	Up
1388392_at	tax1 (human t-cell leukemia virus type i) binding protein 3	Up
1388393_at	proteolipid protein 2 (mapped)	Up
1388401_at	filamin, beta (predicted)	Up
1388408_at	similar to riken cdna 1110020c13	Up
1388422_at	lim and senescent cell antigen like domains 2	Up
1388443_at	cdk2 (cyclin-dependent kinase 2)-associated protein 1 (predicted)	Up
1388449_at	eukaryotic translation elongation factor 1 beta 2 (predicted)	Up
1388455_at	guanine nucleotide binding protein (g protein), gamma 10	Up
1388458_at	replication factor c (activator 1) 4 (predicted)	Up
1388468_at	similar to small protein effector 1 of cdc42	Up
1388478_at	,gb:be108225 /db_xref=gi:8500330 /db_xref=ui-r-bs1-ayw-h-02-0-ui.s1 /clone=ui-r-bs1-ayw-h-02-0-ui /fea=est /cnt=17 /tid=rn.34428.1 /tier=stack /stk=17 /ug=rn.34428 /ug_title=ests	Up
1388481_at	ribosomal protein s28	Up
1388482_at	similar to riken cdna 9130404d14	Up
1388483_at	cofilin 2, muscle (predicted)	Up
1388484_at	ubiquitin-conjugating enzyme e2c (predicted)	Up
1388488_at	lsm3 homolog, u6 small nuclear rna associated (s. cerevisiae) (predicted)	Up
1388494_at	procollagen, type iv, alpha 2 (predicted)	Up
1388514_at	protein phosphatase 1g (formerly 2c), magnesium-dependent, gamma isoform	Up
1388528_at	fibrillarin	Up
1388529_at	rna terminal phosphate cyclase domain 1	Up
1388557_at	complement component 7 (predicted)	Up
1388565_at	spastic paraplegia 21 homolog (human)	Up
1388587_at	immediate early response 3	Up
1388592_at	,gb:bi298958 /db_xref=gi:14975238 /db_xref=ui-r-cv2-chp-e-07-0-ui.s1 /clone=ui-r-cv2-chp-e-07-0-ui /fea=est /cnt=15 /tid=rn.49412.1 /tier=stack /stk=14 /ug=rn.49412 /ug_title=ests	Up
1388622_at	nucleolar protein 5a	Up
1388628_at	integral type i protein	Up
1388629_at	inosine 5-monophosphate dehydrogenase 2	Up
1388645_at	similar to riken cdna 2810409h07	Up
1388650_at	topoisomerase (dna) 2 alpha	Up
1388668_at	methyltransferase like 2 (predicted)	Up
1388682_at	cornichon homolog (drosophila) (predicted)	Up
1388686_at	down syndrome critical region homolog 1 (human)	Up

Supplemental Data Table S8. Continued.

1388696_at	ubiquitin fusion degradation 1-like	Up
1388709_at	similar to wd-repeat protein 43	Up
1388711_at	interleukin 13 receptor, alpha 1	Up
1388715_at	glycyl-trna synthetase	Up
1388726_a_at	,gb:aa800242 /db_xref=gi:2863197 /db_xref=est189739 /clone=rheam85 /fea=est /cnt=80 /tid=rn.34416.2 /tier=stack /stk=16 /ug=rn.34416 /ug_title=ests	Up
1388728_at	lysosomal-associated protein transmembrane 4b	Up
1388745_at	sema domain, immunoglobulin domain (ig), transmembrane domain (tm) and short cytoplasmic domain, (semaphorin) 4a	Up
1388761_at	histone deacetylase 1 (predicted)	Up
1388771_at	cgg triplet repeat binding protein 1 (predicted)	Up
1388772_at	lsm8 homolog, u6 small nuclear rna associated (s. cerevisiae) (predicted)	Up
1388776_at	scotin	Up
1388780_at	telomeric repeat binding factor 2, interacting protein	Up
1388786_at	,gb:bf407452 /db_xref=gi:11395427 /db_xref=ui-r-bj2-bqs-d-07-0-ui.s1 /clone=ui-r-bj2-bqs-d-07-0-ui /fea=est /cnt=15 /tid=rn.7071.1 /tier=stack /stk=11 /ug=rn.7071 /ug_title=ests	Up
1388787_at	similar to hypothetical protein flj13855 (predicted)	Up
1388865_at	protein phosphatase 4, regulatory subunit 2 (predicted)	Up
1388867_at	similar to transcription factor	Up
1388868_at	zinc finger protein 216 (predicted)	Up
1388871_at	ash2 (absent, small, or homeotic)-like (drosophila) (predicted)	Up
1388906_at	similar to novel protein similar to tensin tns	Up
1388913_at	phosphatidic acid phosphatase type 2c	Up
1388924_at	angiopoietin-like protein 4	Up
1388930_at	similar to riken cdna 2310075c12	Up
1388932_at	laminin, alpha 5	Up
1388997_at	adp-ribosylation factor 3	Up
1389047_at	zinc finger protein 451	Up
1389145_at	cdc42 effector protein (rho gtpase binding) 2	Up
1389189_at, 1398294_at	actinin, alpha 1	Up
1389197_at	similar to riken cdna 9630046k23	Up
1389220_at	,gb:be112918 /db_xref=gi:8505023 /db_xref=ui-r-bj1-awa-d-03-0-ui.s1 /clone=ui-r-bj1-awa-d-03-0-ui /fea=est /cnt=9 /tid=rn.30073.1 /tier=stack /stk=8 /ug=rn.30073 /ug_title=ests	Up
1389228_at	similar to riken cdna 2010309e21 (predicted)	Up
1389263_at	retinoic acid induced 14	Up
1389282_at	integrin alpha 3 (predicted)	Up
1389292_at	rab18, member ras oncogene family	Up
1389292_at	similar to rab18	Up
1389294_at	cytoplasmic fmr1 interacting protein 1 (predicted)	Up

Supplemental Data Table S8. Continued.

1389355_at	immediate early response 5	Up
1389390_at	similar to odag protein	Up
1389391_at	similar to solute carrier family 35, member e3	Up
1389408_at	ribonucleotide reductase m2 (mapped)	Up
1389409_at	similar to testis derived transcript	Up
1389446_at	small nuclear ribonucleoprotein polypeptide a' (predicted)	Up
1389454_at	programmed cell death 5 (predicted)	Up
1389518_at	f-box only protein 10 (predicted)	Up
1389520_at	similar to wdr1 protein	Up
1389528_s_at	jun oncogene	Up
1389538_at	nuclear factor of kappa light chain gene enhancer in b-cells inhibitor, alpha	Up
1389555_at	transcription factor 19	Up
1389566_at	cyclin b2	Up
1389668_at	similar to ad024 protein	Up
1389716_at	loc501614	Up
1389815_at	protein phosphatase 1, regulatory (inhibitor) subunit 14b	Up
1389857_at	similar to ww domain binding protein 5	Up
1389885_at	similar to riken cdna 0610025l06	Up
1389911_at	similar to cdna sequence bc019776	Up
1389966_at	procollagen, type vi, alpha 3 (predicted)	Up
1389967_at	adp-ribosylation factor-like 6 interacting protein 1	Up
1389969_at	translocase of outer mitochondrial membrane 40	Up
1389973_a_at	surfeit 1	Up
1389973_a_at	surfeit gene 4 (predicted)	Up
1389980_at	similar to protein hspc163	Up
1390022_at	actin related protein 2/3 complex, subunit 5	Up
1390082_at	huntingtin interacting protein 1	Up
1390116_at	polymerase i and transcript release factor (predicted)	Up
1390177_at	,gb:ai233857 /db_xref=gi:3817737 /db_xref=est230545 /clone=rlucs05 /fea=est /cnt=9 /tid=rn.6397.1 /tier=consend /stk=5 /ug=rn.6397 /ug_title=ests	Up
1390178_at	signal recognition particle receptor, b subunit	Up
1390383_at	adipose differentiation-related protein	Up
1390384_at	similar to histone h2a.x (h2a/x)	Up
1390411_at	claudin 19	Up
1390419_a_at	similar to n33 protein	Up
1390604_s_at	integrin beta 3 binding protein (beta3-endonexin)	Up
1391505_x_at	,gb:bi275261 /db_xref=gi:14886936 /db_xref=ui-r-cx0-bwr-d-11-0-ui.s1 /clone=ui-r-cx0-bwr-d-11-0-ui /fea=est /cnt=5 /tid=rn.24928.1 /tier=consend /stk=2 /ug=rn.24928 /ug_title=ests	Up
1391518_at	similar to 60s ribosomal protein l7a	Up
1392900_at	similar to mkiaa1631 protein	Up

Supplemental Data Table S8. Continued.

1393894_at	cytochrome p450, 4a12	Up
1398315_at	ribosomal protein l15	Up
1398345_at	angiopoietin-like 2	Up
1398347_at	axl receptor tyrosine kinase (predicted)	Up
1398356_at	cleavage and polyadenylation specific factor 5	Up
1398373_at	udp-gal:betaglcnac beta 1,3-galactosyltransferase, polypeptide 3	Up
1398383_at	cytochrome b-561 (predicted)	Up
1398385_at	similar to riken cdna 1500006o09 (predicted)	Up
1398387_at	unknown (protein for mgc:72614)	Up
1398751_at	similar to ribosomal protein s7	Up
1398752_at	selenoprotein	Up
1398756_at	similar to nucleophosmin (npm) (nucleolar phosphoprotein b23) (numatrin) (nucleolar protein no38)	Up
1398756_at, 1399158_a_at, 1398757_at	nucleophosmin 1	Up
1398759_at	transforming growth factor beta 1 induced transcript 4	Up
1398760_at	ribosomal protein l35a	Up
1398762_at	syndecan binding protein	Up
1398765_at	adaptor-related protein complex 2, mu 1 subunit	Up
1398766_at	ribophorin i	Up
1398768_at	retinoblastoma binding protein 7	Up
1398771_at	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	Up
1398775_at	ribosomal protein s15a	Up
1398781_at	atpase, h+ transporting, v1 subunit f	Up
1398786_at	proteasome (prosome, macropain) subunit, beta type 2	Up
1398789_at	ribosomal protein l37	Up
1398797_at	heterogeneous nuclear ribonucleoprotein k	Up
1398798_at	methionine aminopeptidase 2	Up
1398799_at	eukaryotic translation initiation factor 4e	Up
1398800_at	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	Up
1398810_at	pdgfa associated protein 1	Up
1398811_at	jumping translocation breakpoint	Up
1398828_at, 1398829_at	fk506 binding protein 1a	Up
1398831_at	proteasome (prosome, macropain) subunit, beta type 4	Up
1398832_at	nucleolin	Up
1398849_at	h3 histone, family 3b	Up
1398856_at	proteasome (prosome, macropain) subunit, alpha type 2	Up
1398863_at	guanine nucleotide binding protein, beta polypeptide 2	Up
1398871_at	ribosomal protein l17	Up

Supplemental Data Table S8. Continued.

1398872_at	ribosomal protein s13	Up
1398882_at	ribosomal protein s5	Up
1398886_at	similar to selenoprotein h	Up
1398889_at	glutamate receptor, ionotropic, n-methyl d-aspartate-like 1a	Up
1398892_at	niemann pick type c2	Up
1398897_at	ubiquitin-conjugating enzyme e2 variant 1 (predicted)	Up
1398904_at	similar to nono protein	Up
1398904_at	non-pou domain containing, octamer-binding	Up
1398937_at	deah (asp-glu-ala-his) box polypeptide 15 (predicted)	Up
1398952_at	similar to riken cdna 2310036o22	Up
1398952_at	similar to riken cdna 2310036o22	Up
1399019_at	abhydrolase domain containing 4 (predicted)	Up
1399033_at	core binding factor beta	Up
1399050_at	adenylosuccinate synthetase 2, non muscle (predicted)	Up
1399057_at	mortality factor 4 like 1	Up
1399091_at	f-actin capping protein beta subunit	Up
1399108_at	similar to expressed sequence av340375	Up
1367519_at	oxysterol binding protein-like 2	Down
1367548_at	similar to flj00052 protein (predicted)	Down
1367583_at	tumor protein, translationally-controlled 1	Down
1367589_at	aconitase 2, mitochondrial	Down
1367609_at	macrophage migration inhibitory factor	Down
1367638_at	malonyl-coa decarboxylase	Down
1367649_at	paralemmin	Down
1367672_at	hydroxysteroid (17-beta) dehydrogenase 4	Down
1367680_at	acyl-coenzyme a oxidase 1, palmitoyl	Down
1367702_at	acetyl-coenzyme a dehydrogenase, medium chain	Down
1367725_at	serine/threonine-protein kinase pim-3	Down
1367729_at	ornithine aminotransferase	Down
1367755_at	cysteine dioxygenase 1, cytosolic	Down
1367763_at	acetyl-coenzyme a acetyltransferase 1	Down
1367775_at	alpha-methylacyl-coa racemase	Down
1367793_at	d-dopachrome tautomerase	Down
1367798_at	s-adenosylhomocysteine hydrolase	Down
1367838_at	ctl target antigen	Down
1367845_at	neurofilament 3, medium	Down
1367885_at	peroxisomal membrane protein 2	Down
1367905_at	ectonucleotide pyrophosphatase/phosphodiesterase 3	Down
1367952_at	low density lipoprotein receptor-related protein 2	Down
1367969_at	peroxiredoxin 6	Down
1367977_at	synuclein, alpha	Down

Supplemental Data Table S8. Continued.

1367988_at	cytochrome p450, family 2, subfamily c, polypeptide 23	Down
1367995_at	catalase	Down
1368016_at	peroxisomal trans-2-enoyl-coa reductase	Down
1368038_at	synaptojanin 2 binding protein	Down
1368059_at	crystallin, mu	Down
1368060_at	heat-responsive protein 12	Down
1368077_at	fructose-1,6- biphosphatase 1	Down
1368084_at	deoxyribonuclease i	Down
1368085_at	gtp cyclohydrolase i feedback regulator	Down
1368092_at	fumarylacetoacetate hydrolase	Down
1368096_at	rab7, member ras oncogene family-like 1	Down
1368121_at	aldo-keto reductase family 7, member a3 (aflatoxin aldehyde reductase)	Down
1368122_at	ring finger protein 103	Down
1368137_at	microtubule-associated protein tau	Down
1368137_at	hypothetical gene supported by nm_017212	Down
1368139_s_at	alkaline phosphatase, tissue-nonspecific	Down
1368150_at	hypothetical gene supported by nm_031736	Down
1368150_at	solute carrier family 27 (fatty acid transporter), member 2	Down
1368153_a_at	nasal embryonic lhrh factor	Down
1368163_at, 1387084_at	dipeptidylpeptidase 4	Down
1368164_at	biliverdin reductase a	Down
1368180_s_at	glutathione-s-transferase, alpha type2	Down
1368208_at	camello-like 1	Down
1368231_at	signal transducer and activator of transcription 5a	Down
1368245_at	ureidopropionase, beta	Down
1368253_at	guanidinoacetate methyltransferase	Down
1368304_at	flavin containing monooxygenase 3	Down
1368317_at	aquaporin 7	Down
1368329_at	solute carrier family 22 (organic anion transporter), member 6	Down
1368366_at	camello-like 2	Down
1368372_at	steroid sulfatase	Down
1368390_at	v-raf oncogene homolog 1 (murine sarcoma 3611 virus)	Down
1368397_at	udp glycosyltransferase 2 family, polypeptide b4	Down
1368397_at	udp-glucuronosyltransferase 2 family, member 5	Down
1368431_at	hepsin	Down
1368440_at	solute carrier family 3, member 1	Down
1368442_at	coagulation factor 2	Down
1368467_at	cytochrome p450, family 4, subfamily f, polypeptide 2	Down
1368509_at	bardet-biedl syndrome 2 (human)	Down
1368562_at	sulfotransferase family 4a, member 1	Down

Supplemental Data Table S8. Continued.

1368563_at	aspartoacylase	Down
1368575_at	solute carrier family 6 (neurotransmitter transporter), member 18	Down
1368583_a_at	histidine-rich glycoprotein	Down
1368627_at	regucalcin	Down
1368651_at	pyruvate kinase, liver and red blood cell	Down
1368661_at	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2	Down
1368784_at	apobec-1 complementation factor	Down
1368794_at	3-hydroxyanthranilate 3,4-dioxygenase	Down
1368814_at	aldehyde dehydrogenase family 6, subfamily a1	Down
1368852_at, 1398819_at	dnaj-like protein	Down
1368915_at	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	Down
1368957_at	guanine nucleotide binding protein, gamma 7	Down
1368963_at	max interacting protein 1	Down
1369065_a_at, 1370426_a_at	atpase, ca++ transporting, cardiac muscle, slow twitch 2	Down
1369124_at	5-hydroxytryptamine (serotonin) receptor 2a	Down
1369159_at	androgen receptor	Down
1369169_at	solute carrier family 23 (nucleobase transporters), member 1	Down
1369259_at	deiodinase, iodothyronine, type i	Down
1369289_at, 1382496_at	hepatocyte nuclear factor 4, alpha	Down
1369318_at	fragile histidine triad gene	Down
1369401_at	solute carrier family 21, member 13	Down
1369450_at	integral membrane transport protein ust5r	Down
1369453_at	epsin 1	Down
1369491_at	d-amino acid oxidase	Down
1369494_a_at	growth hormone releasing hormone receptor	Down
1369625_at, 1387651_at	aquaporin 1	Down
1369629_at	adenosine kinase	Down
1369632_a_at	atp-binding cassette, sub-family c (cftr/mrp), member 8	Down
1369680_at	solute carrier family 2 (facilitated glucose transporter), member 13	Down
1369864_a_at	serine dehydratase	Down
1369986_at	hydroxyacyl glutathione hydrolase	Down
1370032_at	erm-binding phosphoprotein	Down
1370036_at	sulfite oxidase	Down
1370067_at	malic enzyme 1	Down
1370144_at	similar to gtp-binding protein ngb	Down
1370144_at	gtp binding protein 4	Down
1370144_at, 1372869_at	similar to gtp-binding protein ngb	Down

Supplemental Data Table S8. Continued.

1370147_at	2-amino-3-carboxymuconate-6-semialdehyde decarboxylase	Down
1370163_at	ornithine decarboxylase 1	Down
1370166_at, 1370167_at	syndecan 2	Down
1370275_at	atp synthase, h+ transporting, mitochondrial f1 complex, beta polypeptide	Down
1370329_at, 1387913_at	cytochrome p450, family 2, subfamily d, polypeptide 22	Down
1370333_a_at	insulin-like growth factor 1	Down
1370336_at	pregnancy-induced growth inhibitor	Down
1370365_at	glutathione synthetase	Down
1370367_at	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system xag), member 1	Down
1370379_at	protease, serine, 8 (prostasin)	Down
1370446_at	non-metastatic cells 7, protein expressed in	Down
1370474_at, 1387983_at	thyroid hormone receptor beta	Down
1370547_at	pregnancy-zone protein	Down
1370609_a_at	solute carrier family 16 (monocarboxylic acid transporters), member 7	Down
1370613_s_at	udp glycosyltransferase 1 family, polypeptide a8	Down
1370613_s_at	udp glycosyltransferase 1 family polypeptide a11	Down
1370613_s_at	udp glycosyltransferase 1 family, polypeptide a1	Down
1370613_s_at	udp glycosyltransferase 1 family, polypeptide a7	Down
1370613_s_at	udp glycosyltransferase 1 family, polypeptide a5	Down
1370613_s_at	udp glycosyltransferase 1 family polypeptide a2	Down
1370613_s_at	udp glycosyltransferase 1 family, polypeptide a3	Down
1370614_s_at	serine/threonine kinase 39, ste20/sps1 homolog (yeast)	Down
1370688_at, 1372523_at	glutamate-cysteine ligase, catalytic subunit	Down
1370715_at	similar to mkiaa0998 protein	Down
1370724_a_at	nuclear factor i/a	Down
1370725_a_at, 1386944_a_at	glucose-6-phosphatase, catalytic	Down
1370789_a_at	prolactin receptor	Down
1370814_at	dehydrogenase/reductase (sdr family) member 4	Down
1370818_at	2-4-dienoyl-coenzyme a reductase 2, peroxisomal	Down
1370821_at	thiopurine methyltransferase	Down
1370824_at	solute carrier family 38, member 3	Down
1370853_at	calcium/calmodulin-dependent protein kinase ii inhibitor 1	Down
1370884_at	sepiapterin reductase	Down
1370897_at	branched chain ketoacid dehydrogenase e1, alpha polypeptide	Down
1370929_at	low density lipoprotein receptor-related protein associated protein 1	Down
1370936_at	dimethylglycine dehydrogenase precursor	Down

1370943_at	sulfotransferase family, cytosolic, 1c, member 1 (predicted)	Down
1370991_at	camello-like 3	Down
1371012_at	2-hydroxyphytanoyl-coenzyme a lyase	Down
1371185_at	integrin, alpha 6	Down
1371309_at	testis enhanced gene transcript	Down
1371321_at	cytochrome c oxidase, subunit vib (predicted)	Down
1371350_at	similar to s-adenosylmethionine synthetase gamma form (methionine adenosyltransferase) (adomet synthetase) (mat-ii)	Down
1371359_at	myeloid leukemia factor 2 (predicted)	Down
1371380_at	pyruvate dehydrogenase e1 alpha 1	Down
1371389_at	hypothetical loc306766	Down
1371405_at	similar to hypothetical protein mgc52110	Down
1371421_at	similar to flj40243 protein (predicted)	Down
1371483_at	nicotinamide nucleotide transhydrogenase (mapped)	Down
1371496_at	,gb:ai178804 /db_xref=gi:3729442 /db_xref=est222486 /clone=rspbm81 /fea=est /cnt=23 /tid=rn.13458.1 /tier=stack /stk=22 /ug=rn.13458 /ug_title=ests	Down
1371584_at	transient receptor potential cation channel, subfamily c, member 4 associated protein	Down
1371599_at	lrrgt00097	Down
1371730_at	similar to riken cdna 1300002a08	Down
1371763_at	similar to riken cdna 4931406c07	Down
1371769_at	secretory carrier membrane protein 2	Down
1371824_at	adenylate kinase 3-like 1	Down
1371835_at	protein kinase, camp dependent, catalytic, beta (predicted)	Down
1371886_at	carnitine acetyltransferase	Down
1371912_at	nadh dehydrogenase (ubiquinone) fe-s protein 7	Down
1371913_at	transforming growth factor, beta induced	Down
1371916_at	selenoprotein x 1 (predicted)	Down
1371942_at	similar to glutathione s-transferase, theta 3	Down
1371997_at	aldo-keto reductase family 1, member e1	Down
1372018_at	cdc42-binding protein kinase beta	Down
1372076_at	hepatitis b virus x interacting protein (predicted)	Down
1372107_at	four and a half lim domains 1	Down
1372132_at	cndp dipeptidase 2 (metallopeptidase m20 family)	Down
1372161_at	similar to putative emu2 protein	Down
1372170_at	aminoacylase 1	Down
1372199_at, 1372475_at	pten induced putative kinase 1 (predicted)	Down
1372208_at	protein phosphatase 1, regulatory (inhibitor) subunit 1b	Down
1372264_at	phosphoenolpyruvate carboxykinase 1	Down
1372306_at	ethylmalonic encephalopathy 1 (predicted)	Down
1372319_at	zinc fingers and homeoboxes 3	Down

Supplemental Data Table S8. Continued.

1372323_at	sarcosine dehydrogenase	Down
1372324_at	similar to thyroid hormone receptor interactor 3	Down
1372341_at	similar to riken cdna c330005l02 (predicted)	Down
1372437_at	s-phase kinase-associated protein 1a	Down
1372438_at	similar to nit protein 2	Down
1372612_at	dynein light chain-2	Down
1372637_at	,gb:ai169241 /db_xref=gi:3705549 /db_xref=est215076 /clone=rkibp21 /fea=est /cnt=12 /tid=rn.14890.1 /tier=stack /stk=11 /ug=rn.14890 /ug_title=ests, weakly similar to pn0109 keratin-like protein - rat (r.norvegicus)	Down
1372638_at	rho guanine nucleotide exchange factor 7	Down
1372658_at	desmuslin	Down
1372744_at	plakophilin 4 (predicted)	Down
1372790_at	malate dehydrogenase 1, nad (soluble)	Down
1372841_at	deleted in polyposis 1-like 1	Down
1372860_at	similar to phospholysine phosphohistidine inorganic pyrophosphate phosphata (5m590)	Down
1373057_at	prosapip1 protein	Down
1373110_at	,gb:ai407487 /db_xref=gi:4250991 /db_xref=est235776 /clone=rovdu14 /fea=est /cnt=13 /tid=rn.1452.1 /tier=stack /stk=9 /ug=rn.1452 /ug_title=ests	Down
1373170_at	g protein pathway suppressor 2 (predicted)	Down
1373178_at	,gb:aa945183 /db_xref=gi:4132515 /db_xref=est200682 /clone=rliah59 /fea=est /cnt=11 /tid=rn.40381.1 /tier=stack /stk=9 /ug=rn.40381 /ug_title=ests	Down
1373180_at	,gb:ai227919 /db_xref=gi:3811806 /db_xref=est224614 /clone=rbrcn61 /fea=est /cnt=11 /tid=rn.17029.1 /tier=stack /stk=9 /ug=rn.17029 /ug_title=ests	Down
1373188_at	sodium channel, voltage-gated, type iv, beta	Down
1373240_at	dehydrogenase/reductase (sdr family) member 3	Down
1373304_at	alpha-n-acetylglucosaminidase	Down
1373365_at	similar to ump-cmp kinase	Down
1373420_at	evolutionarily conserved signaling intermediate in toll pathway	Down
1373425_at	similar to cdc-like kinase 2	Down
1373521_at	similar to riken cdna d430044g18	Down
1373542_at	sphingosine kinase 2	Down
1373590_at	stomatin	Down
1373625_at	serine hydroxymethyl transferase 1 (soluble)	Down
1373645_at	matrix metalloproteinase 1a (interstitial collagenase) (predicted)	Down
1373675_at	glutaredoxin 2 (thioltransferase)	Down
1373689_at	,gb:bg379711 /db_xref=gi:13304183 /db_xref=ui-r-cs0-btj-c-09-0-ui.s1 /clone=ui-r-cs0-btj-c-09-0-ui /fea=est /cnt=9 /tid=rn.23611.1 /tier=stack /stk=8 /ug=rn.23611 /ug_title=ests	Down
1373888_at	adaptor-related protein complex 3, beta 1 subunit (predicted)	Down

Supplemental Data Table S8. Continued.

1373896_at	synaptotagmin 1	Down
1373933_at	rap guanine nucleotide exchange factor (gef) 2 (predicted)	Down
1373938_at	similar to hypothetical protein mgc47001	Down
1374022_at	,gb:ai406707 /db_xref=gi:4250211 /db_xref=est234994 /clone=rovdv56 /fea=est /cnt=9 /tid=rn.18035.1 /tier=stack /stk=7 /ug=rn.18035 /ug_title=ests	Down
1374162_at	,gb:ai112255 /db_xref=gi:3512204 /db_xref=ui-r-y0-mh-h-09-0-ui.s1 /clone=ui-r-y0-mh-h-09-0-ui /fea=est /cnt=8 /tid=rn.17670.1 /tier=stack /stk=7 /ug=rn.17670 /ug_title=ests	Down
1374179_at	rt1 class i, a3	Down
1374217_at, 1375674_at	similar to chromosome 16 open reading frame 5	Down
1374241_at	,gb:ai406271 /db_xref=gi:4249775 /db_xref=est234557 /clone=rbrdl82 /fea=est /cnt=7 /tid=rn.23363.1 /tier=stack /stk=7 /ug=rn.23363 /ug_title=ests	Down
1374244_at	ab2-060	Down
1374459_at	asparagine-linked glycosylation 2 homolog (yeast, alpha-1,3-mannosyltransferase) (predicted)	Down
1374478_at	similar to riken cdna 2610528j11 (predicted)	Down
1374625_at	hairy and enhancer of split 6 (drosophila)	Down
1374628_at	crystallin, zeta	Down
1374641_at	,gb:bf397653 /db_xref=gi:11382637 /db_xref=ui-r-bs2-bed-a-09-0-ui.s1 /clone=ui-r-bs2-bed-a-09-0-ui /fea=est /cnt=8 /tid=rn.40613.1 /tier=stack /stk=6 /ug=rn.40613 /ug_title=ests	Down
1374709_at	,gb:ai406795 /db_xref=gi:4250299 /db_xref=est235082 /clone=rbrdi44 /fea=est /cnt=9 /tid=rn.19878.1 /tier=stack /stk=6 /ug=rn.19878 /ug_title=ests	Down
1374959_at	nad(p)h dehydrogenase, quinone 2	Down
1375024_at	similar to riken cdna 5230400j09	Down
1375120_at	inhibitor of dna binding 4	Down
1375138_at	tissue inhibitor of metalloproteinase 3 (sorsby fundus dystrophy, pseudoinflammatory)	Down
1375146_at	similar to riken cdna 3010027g13	Down
1375206_at	hypothetical loc287466	Down
1375247_at, 1388644_at	monoglyceride lipase	Down
1375267_at	peptidylprolyl isomerase c	Down
1375288_at	gcn1 general control of amino-acid synthesis 1-like 1 (yeast) (predicted)	Down
1375445_at	,gb:bg375795 /db_xref=gi:13300267 /db_xref=ui-r-cs0-btf-e-06-0-ui.s1 /clone=ui-r-cs0-btf-e-06-0-ui /fea=est /cnt=11 /tid=rn.24084.1 /tier=stack /stk=8 /ug=rn.24084 /ug_title=ests	Down
1375458_at	asparaginase-like sperm autoantigen	Down
1375596_at	transient receptor potential cation channel, subfamily m, member 1	Down
1375642_at	ubiquitin-conjugating enzyme e2b, rad6 homolog (s. cerevisiae)	Down
1375944_at	acetyl-coenzyme a synthetase 2 (adp forming) (predicted)	Down

Supplemental Data Table S8. Continued.

1375997_at	,gb:aa799503 /db_xref=gi:2862458 /db_xref=est189000 /clone=rheab81 /fea=est /cnt=8 /tid=rn.3768.1 /tier=consend /stk=5 /ug=rn.3768 /ug_title=ests	Down
1376073_at	sel1 (suppressor of lin-12) 1 homolog (c. elegans)	Down
1376078_at	,gb:bi296274 /db_xref=gi:14960555 /db_xref=ui-r-dk0-cey-d-07-0-ui.s1 /clone=ui-r-dk0-cey-d-07-0-ui /fea=est /cnt=7 /tid=rn.22415.1 /tier=consend /stk=5 /ug=rn.22415 /ug_title=ests	Down
1376128_at	,gb:ai103937 /db_xref=gi:3704874 /db_xref=est213226 /clone=rhebv35 /fea=est /cnt=6 /tid=rn.17851.1 /tier=consend /stk=5 /ug=rn.17851 /ug_title=ests	Down
1376163_at	similar to expressed sequence ai649392	Down
1376209_at	similar to hypothetical protein supported by al449243 (predicted)	Down
1376337_at	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	Down
1376404_at	,gb:ai639317 /db_xref=gi:4700351 /db_xref=rx04857s /clone=rx04857 /fea=est /cnt=5 /tid=rn.43513.1 /tier=consend /stk=5 /ug=rn.43513 /ug_title=ests	Down
1376592_at	methylmalonyl coa epimerase (predicted)	Down
1376605_at	solute carrier family 17 (anion/sugar transporter), member 5	Down
1376702_at	megalencephalic leukoencephalopathy with subcortical cysts 1 (predicted)	Down
1376709_at	solute carrier family 39 (metal ion transporter), member 8	Down
1376728_at	protein phosphatase 1, regulatory (inhibitor) subunit 8 (predicted)	Down
1376746_at, 1382061_at	lactate dehydrogenase d	Down
1376765_at	similar to maestro	Down
1376773_at	,gb:ai406968 /db_xref=gi:4250472 /db_xref=est235256 /clone=rovdw86 /fea=est /cnt=6 /tid=rn.19462.1 /tier=consend /stk=4 /ug=rn.19462 /ug_title=ests	Down
1376808_at	,gb:bg672572 /db_xref=gi:13894671 /db_xref=drncle11 /clone=drncle11 /fea=est /cnt=6 /tid=rn.21871.1 /tier=consend /stk=4 /ug=rn.21871 /ug_title=ests	Down
1376824_at	similar to riken cdna 1700027m01	Down
1376852_at	methylcrotonoyl-coenzyme a carboxylase 1 (alpha)	Down
1377048_at	similar to cdna sequence bc021917	Down
1377056_at	,gb:bf393907 /db_xref=gi:11378770 /db_xref=ui-r-ca0-bgw-e-02-0-ui.s1 /clone=ui-r-ca0-bgw-e-02-0-ui /fea=est /cnt=5 /tid=rn.46805.1 /tier=consend /stk=4 /ug=rn.46805 /ug_title=ests	Down
1377088_at	similar to riken cdna 2310046k01	Down
1377265_at	similar to hccs protein	Down
1377351_at	sushi domain containing 3 (predicted)	Down
1377966_at	,gb:bi275560 /db_xref=gi:14919591 /db_xref=ui-r-cx0-bwy-g-08-0-ui.s1 /clone=ui-r-cx0-bwy-g-08-0-ui /fea=est /cnt=5 /tid=rn.22923.1 /tier=consend /stk=3 /ug=rn.22923 /ug_title=ests	Down
1379243_at	nadh dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (b14) (predicted)	Down
1379456_at	mitochondrial carrier triple repeat 1	Down

Supplemental Data Table S8. Continued.

1382683_a_at	,gb:aa891943 /db_xref=gi:3018822 /db_xref=est195746 /clone=rkiai86 /fea=est /cnt=1 /tid=rn.3564.2 /tier=consend /stk=1 /ug=rn.3564 /ug_title=ests	Down
1383161_a_at	,gb:ai008646 /db_xref=gi:4132919 /db_xref=est203097 /clone=rembb18 /fea=est /cnt=8 /tid=rn.3800.3 /tier=consend /stk=0 /ug=rn.3800 /ug_title=ests	Down
1384970_at	similar to riken cdna 5330437i02 gene	Down
1385088_at	hypothetical loc304650 (predicted)	Down
1385241_at	stromal antigen 1 (predicted)	Down
1386280_at	similar to riken cdna 0610006f02	Down
1386701_at	,gb:bf565038 /db_xref=gi:11674768 /db_xref=ui-r-bu0-ams-a-01-0-ui.r1 /clone=ui-r-bu0-ams-a-01-0-ui /fea=est /cnt=1 /tid=rn.48004.2 /tier=consend /stk=0 /ug=rn.48004 /ug_title=ests	Down
1386885_at	enoyl coenzyme a hydratase 1, peroxisomal	Down
1386904_a_at	cytochrome b-5	Down
1386909_a_at	voltage-dependent anion channel 1	Down
1386916_at	aconitase 1	Down
1386917_at	pyruvate carboxylase	Down
1386938_at	alanyl (membrane) aminopeptidase	Down
1386942_at	cis-golgi matrix protein gm130	Down
1386954_at	adenylate kinase 2	Down
1387019_at	atp synthase, h+ transporting, mitochondrial f0 complex, subunit e	Down
1387022_at	aldehyde dehydrogenase family 1, member a1	Down
1387023_at	glutathione s-transferase, mu type 3	Down
1387121_a_at	n-myc downstream regulated gene 2	Down
1387139_at	hydroxyacid oxidase 2 (long chain)	Down
1387158_at	meprin 1 beta	Down
1387178_a_at	cystathionine beta synthase	Down
1387232_at	bone morphogenetic protein 4	Down
1387253_at	guanylate cyclase activator 2b	Down
1387295_at	solute carrier family 6 (neurotransmitter transporter, betaine/gaba), member 12	Down
1387303_at	solute carrier family 22 (organic cation transporter), member 2	Down
1387328_at	cytochrome p450, subfamily iic (mephenytoin 4-hydroxylase)	Down
1387336_at	n-acetyltransferase 8 (camello like)	Down
1387375_at	ketohexokinase	Down
1387382_at	histamine n-methyltransferase	Down
1387519_at	vesicle-associated membrane protein 1	Down
1387531_at	methionine sulfoxide reductase a	Down
1387542_at	solute carrier family 9, member 3	Down
1387567_at	solute carrier family (organic anion transporter) member 3	Down
1387567_at	hypothetical gene supported by nm_017111	Down
1387669_a_at	epoxide hydrolase 1, microsomal	Down

Supplemental Data Table S8. Continued.

1387685_at	frequenin homolog (drosophila)	Down
1387698_at	potassium inwardly rectifying channel, subfamily j, member 11	Down
1387703_a_at	ubiquitin specific protease 2	Down
1387783_a_at	acetyl-coenzyme a acyltransferase 1	Down
1387799_at	fxyd domain-containing ion transport regulator 2	Down
1387857_at	syntaxin 7	Down
1387861_at	amino-terminal enhancer of split	Down
1387867_at	aldehyde dehydrogenase family 9, subfamily a1	Down
1387878_at	glutamate dehydrogenase 1	Down
1387971_a_at	mitogen activated protein kinase 8 interacting protein	Down
1387974_a_at	kidney specific organic anion transporter	Down
1388120_at	programmed cell death 6 interacting protein	Down
1388145_at	tenascin xa	Down
1388163_at	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	Down
1388172_at	solute carrier family 22 (organic anion/cation transporter), member 9	Down
1388324_at	nitrilase 1	Down
1388327_at	similar to dna segment, chr 10, erato doi 214, expressed (predicted)	Down
1388361_at	nadh dehydrogenase (ubiquinone) 1 beta subcomplex, 10 (predicted)	Down
1388402_at	similar to 2410001h17rik protein (predicted)	Down
1388403_at	similar to nadp+-specific isocitrate dehydrogenase	Down
1388435_at	crystallin, gamma s	Down
1388486_at	dipeptidylpeptidase 8 (predicted)	Down
1388579_at	similar to hypothetical gene mgc19595 (predicted)	Down
1388734_at	,gb:aa894193 /db_xref=gi:3021072 /db_xref=est197996 /clone=rspas42 /fea=est /cnt=13 /tid=rn.11542.1 /tier=stack /stk=12 /ug=rn.11542 /ug_title=ests	Down
1388750_at	transferrin receptor	Down
1388751_at	rna binding motif protein 24 (predicted)	Down
1388778_at	,gb:bf284876 /db_xref=gi:11215946 /db_xref=est449467 /clone=rgiex35 /fea=est /cnt=15 /tid=rn.17629.1 /tier=stack /stk=11 /ug=rn.17629 /ug_title=ests	Down
1388788_at	glutaryl-coenzyme a dehydrogenase (predicted)	Down
1388908_at	peroxisomal delta3, delta2-enoyl-coenzyme a isomerase	Down
1388909_at	similar to cdna sequence bc019806 (predicted)	Down
1389059_at	lymphoblastic leukemia derived sequence 1	Down
1389060_at	suppressor of cytokine signaling 7 (predicted)	Down
1389066_at	down syndrome critical region gene 1-like 1	Down
1389109_at	phosphatidylinositol-4-phosphate 5-kinase, type ii, alpha	Down
1389113_at	similar to hypothetical protein mgc32471 (predicted)	Down
1389114_at	similar to hypothetical protein mgc59076	Down

Supplemental Data Table S8. Continued.

1389139_at	similar to ttc15 protein	Down
1389166_at	calcium and integrin binding family member 2	Down
1389219_at	similar to serine/threonine kinase	Down
1389251_at	nudix (nucleoside diphosphate linked moiety x)-type motif 7 (predicted)	Down
1389256_at	,gb:bg381256 /db_xref=gi:13305728 /db_xref=ui-r-ct0-bui-a-09-0-ui.s1 /clone=ui-r-ct0-bui-a-09-0-ui /fea=est /cnt=9 /tid=rn.1630.1 /tier=stack /stk=8 /ug=rn.1630 /ug_title=ests	Down
1389310_at	,gb:bf400694 /db_xref=gi:11388669 /db_xref=ui-r-ca0-bhe-d-05-0-ui.s1 /clone=ui-r-ca0-bhe-d-05-0-ui /fea=est /cnt=12 /tid=rn.7568.1 /tier=stack /stk=7 /ug=rn.7568 /ug_title=ests	Down
1389319_at	,gb:aa800719 /db_xref=gi:2863674 /db_xref=est190216 /clone=rluak63 /fea=est /cnt=13 /tid=rn.6624.1 /tier=stack /stk=7 /ug=rn.6624 /ug_title=ests	Down
1389321_at	,gb:bi292917 /db_xref=gi:14953904 /db_xref=ui-r-do0-cix-b-20-0-ui.s1 /clone=ui-r-do0-cix-b-20-0-ui /fea=est /cnt=12 /tid=rn.19306.1 /tier=stack /stk=7 /ug=rn.19306 /ug_title=ests	Down
1389330_at	solute carrier family 5 (sodium/glucose cotransporter), member 2	Down
1389433_at	mckusick-kaufman syndrome protein	Down
1389466_at	ankyrin 3, epithelial isoform g	Down
1389491_at	sideroflexin 5	Down
1389516_at	similar to sperm 1 pou-domain transcription factor (sprm-1) (predicted)	Down
1389522_at	similar to pleckstrin homology domain containing, family a member 6	Down
1389527_at	promethin	Down
1389540_at	tg interacting factor	Down
1389548_at	alcohol dehydrogenase, iron containing, 1	Down
1389549_at	proline synthetase co-transcribed (predicted)	Down
1389551_at, 1390851_at	lactamase, beta 2	Down
1389632_at	rho-related btb domain containing 1 (predicted)	Down
1389680_at	elongation factor rna polymerase ii 2 (predicted)	Down
1389704_at	,gb:aa850490 /db_xref=gi:2938030 /db_xref=est193257 /clone=rovag33 /fea=est /cnt=7 /tid=rn.7010.1 /tier=stack /stk=6 /ug=rn.7010 /ug_title=ests	Down
1389785_at	similar to riken cdna 0610006h10 gene	Down
1389833_at	sulfatase modifying factor 1 (predicted)	Down
1390121_at	glis family zinc finger 2 (predicted)	Down
1390131_at	serine racemase	Down
1390285_at	similar to bc026645 protein	Down
1390296_at	protein kinase inhibitor, gamma	Down
1390416_at	solute carrier family 25, member 30	Down
1390556_at	,gb:bf408801 /db_xref=gi:11396776 /db_xref=ui-r-bt1-bne-e-10-0-ui.s1 /clone=ui-r-bt1-bne-e-10-0-ui /fea=est /cnt=5 /tid=rn.18441.1 /tier=consend /stk=4 /ug=rn.18441 /ug_title=ests	Down

Supplemental Data Table S8. Continued.

1390569_at	similar to carnosinase 1	Down
1392476_at	germinal histone h4 gene	Down
1392476_at	similar to germinal histone h4 gene	Down
1393061_at	similar to cdna sequence bc021608	Down
1393221_at	similar to 20-alpha-hydroxysteroid dehydrogenase	Down
1393417_at	similar to paralemmin 2	Down
1398255_at	solute carrier family 15 (h+/peptide transporter), member 2	Down
1398269_at	netrin 1	Down
1398282_at	kynureninase (l-kynurenine hydrolase)	Down
1398296_at	membrane interacting protein of rgs16	Down
1398341_at	hypothetical loc287661	Down
1398343_at	dnaj (hsp40) homolog, subfamily a, member 4	Down
1398348_at	similar to dimethylarginine dimethylaminohydrolase 1; ng,ng dimethylarginine dimethylaminohydrolase	Down
1398447_at	,gb:aa801323 /db_xref=gi:4131596 /db_xref=est190820 /clone=rplab89 /fea=est /cnt=8 /tid=rn.22049.1 /tier=consend /stk=4 /ug=rn.22049 /ug_title=ests	Down
1398612_at	aldo-keto reductase family 1, member c12 (predicted)	Down
1398807_at	protein phosphatase 1b, magnesium dependent, beta isoform	Down
1398976_at	nuclear receptor co-repressor 1	Down
1398977_at	insulin degrading enzyme	Down
1399109_at	,gb:bi281673 /db_xref=gi:14931647 /db_xref=ui-r-ct0s-cav-b-07-0-ui.s1 /clone=ui-r-ct0s-cav-b-07-0-ui /fea=est /cnt=6 /tid=rn.7769.1 /tier=consend /stk=4 /ug=rn.7769 /ug_title=ests	Down
1399153_at	rab5b, member ras oncogene family (predicted)	Down

Supplemental Data Table S9. Enriched Gene Ontology Terms among PUR-Induced Renal Differential Gene Expression as Determined by Seaching the Gene Ontology and Pathway Databases.

Category	Term	Count	P-Value	Direction
GOTERM_BP_ALL	acetyl-CoA catabolic process	5	6.30E-03	Down
GOTERM_BP_ALL	acetyl-CoA metabolic process	8	3.80E-04	Down
GOTERM_BP_ALL	actin cytoskeleton organization and biogenesis	29	8.40E-06	Up
GOTERM_BP_ALL	actin filament polymerization	11	3.40E-06	Up
GOTERM_BP_ALL	actin filament-based process	29	2.50E-05	Up
GOTERM_BP_ALL	actin polymerization and/or depolymerization	14	2.30E-06	Up
GOTERM_BP_ALL	acute inflammatory response	12	4.70E-02	Up
GOTERM_BP_ALL	aging	8	5.00E-02	Up
GOTERM_BP_ALL	alcohol biosynthetic process	6	5.50E-03	Down
GOTERM_BP_ALL	aldehyde metabolic process	4	1.60E-02	Down
GOTERM_BP_ALL	amine biosynthetic process	9	5.20E-03	Down
GOTERM_BP_ALL	amine catabolic process	13	1.50E-06	Down
GOTERM_BP_ALL	amine metabolic process	37	6.20E-09	Down
GOTERM_BP_ALL	amino acid and derivative metabolic process	37	1.30E-09	Down
GOTERM_BP_ALL	amino acid biosynthetic process	6	1.70E-02	Down
GOTERM_BP_ALL	amino acid catabolic process	13	7.20E-08	Down
GOTERM_BP_ALL	amino acid derivative metabolic process	14	2.20E-04	Down
GOTERM_BP_ALL	amino acid metabolic process	29	1.20E-08	Down
COG_ONTOLOGY	Amino acid transport and metabolism	11	4.60E-03	Down
GOTERM_BP_ALL	anatomical structure development	148	2.00E-03	Up
GOTERM_BP_ALL	anatomical structure morphogenesis	78	4.60E-02	Up
KEGG_PATHWAY	Androgen and estrogen metabolism	10	5.60E-05	Down
GOTERM_BP_ALL	angiogenesis	15	4.10E-02	Up
GOTERM_BP_ALL	anti-apoptosis	22	2.30E-03	Up
GOTERM_BP_ALL	antigen processing and presentation	10	1.80E-02	Up
GOTERM_BP_ALL	antigen processing and presentation of peptide antigen	8	2.20E-02	Up
GOTERM_BP_ALL	aromatic amino acid family metabolic process	4	1.90E-02	Down
GOTERM_BP_ALL	aromatic compound catabolic process	4	8.20E-03	Down
GOTERM_BP_ALL	aromatic compound metabolic process	17	6.30E-06	Down

Supplemental Data Table S9. Continued.

GOTERM_BP_ALL	aspartate family amino acid metabolic process	4	1.60E-02	Down
KEGG_PATHWAY	B cell receptor signaling pathway	11	9.50E-03	Up
KEGG_PATHWAY	beta-Alanine metabolism	5	1.10E-02	Down
GOTERM_BP_ALL	biogenic amine metabolic process	9	5.70E-03	Down
GOTERM_BP_ALL	biological adhesion	41	4.90E-02	Up
GOTERM_BP_ALL	biological regulation	245	3.50E-02	Up
GOTERM_BP_ALL	biopolymer catabolic process	22	4.40E-02	Up
GOTERM_BP_ALL	biosynthetic process	102	5.20E-04	Up
GOTERM_BP_ALL	biosynthetic process	48	3.90E-02	Down
SP_PIR_KEYWORDS	blood coagulation	6	3.00E-02	Up
GOTERM_BP_ALL	blood vessel morphogenesis	18	3.20E-02	Up
GOTERM_BP_ALL	bone remodeling	16	5.00E-02	Up
GOTERM_BP_ALL	branched chain family amino acid catabolic process	3	2.50E-02	Down
GOTERM_BP_ALL	branched chain family amino acid metabolic process	3	4.90E-02	Down
KEGG_PATHWAY	Carbon fixation	4	4.30E-02	Down
GOTERM_BP_ALL	carboxylic acid metabolic process	59	2.20E-17	Down
GOTERM_BP_ALL	catabolic process	36	7.20E-05	Down
GOTERM_BP_ALL	cell adhesion	41	4.90E-02	Up
KEGG_PATHWAY	Cell Communication	14	1.00E-02	Up
KEGG_PATHWAY	Cell cycle	18	8.60E-04	Up
SP_PIR_KEYWORDS	cell cycle	19	3.10E-02	Up
GOTERM_BP_ALL	cell cycle	43	3.50E-02	Up
GOTERM_BP_ALL	cell death	60	1.90E-02	Up
GOTERM_BP_ALL	cell differentiation	115	1.80E-02	Up
GOTERM_BP_ALL	cell division	19	4.20E-04	Up
SP_PIR_KEYWORDS	cell division	14	2.80E-03	Up
GOTERM_BP_ALL	cell migration	29	9.70E-03	Up
GOTERM_BP_ALL	cell morphogenesis	43	1.60E-02	Up
GOTERM_BP_ALL	cell motility	47	1.20E-05	Up
GOTERM_BP_ALL	cell projection biogenesis	8	2.50E-02	Up

Supplemental Data Table S9. Continued.

GOTERM_BP_ALL	cell proliferation	66	5.50E-03	Up
GOTERM_BP_ALL	cellular biosynthetic process	89	1.50E-05	Up
GOTERM_BP_ALL	cellular biosynthetic process	41	1.30E-02	Down
GOTERM_BP_ALL	cellular catabolic process	34	8.90E-06	Down
GOTERM_BP_ALL	cellular component assembly	48	6.70E-04	Up
GOTERM_BP_ALL	cellular component organization and biogenesis	181	3.80E-05	Up
GOTERM_BP_ALL	cellular developmental process	115	1.80E-02	Up
GOTERM_BP_ALL	cellular lipid metabolic process	32	3.80E-04	Down
GOTERM_BP_ALL	cellular macromolecule metabolic process	213	4.90E-09	Up
GOTERM_BP_ALL	cellular metabolic process	366	1.60E-05	Up
GOTERM_BP_ALL	cellular process	525	6.70E-05	Up
GOTERM_BP_ALL	cellular protein catabolic process	16	1.50E-02	Up
GOTERM_BP_ALL	cellular protein metabolic process	209	9.30E-09	Up
GOTERM_BP_ALL	cellular response to hormone stimulus	3	4.00E-02	Down
GOTERM_BP_ALL	cellular response to insulin stimulus	3	4.00E-02	Down
GOTERM_BP_ALL	cellular structure morphogenesis	43	1.60E-02	Up
GOTERM_BP_ALL	chromosome organization and biogenesis	21	3.10E-02	Up
KEGG_PATHWAY	Citrate cycle (TCA cycle)	5	1.30E-02	Down
GOTERM_BP_ALL	coenzyme biosynthetic process	8	8.30E-03	Down
GOTERM_BP_ALL	coenzyme catabolic process	5	7.50E-03	Down
GOTERM_BP_ALL	coenzyme metabolic process	19	1.00E-05	Down
GOTERM_BP_ALL	cofactor biosynthetic process	8	1.90E-02	Down
GOTERM_BP_ALL	cofactor catabolic process	7	5.20E-04	Down
GOTERM_BP_ALL	cofactor metabolic process	22	3.90E-06	Down
GOTERM_BP_ALL	complement activation, classical pathway	5	3.90E-02	Up
KEGG_PATHWAY	Complement and coagulation cascades	10	2.10E-02	Up
SP_PIR_KEYWORDS	complement pathway	5	2.60E-02	Up
GOTERM_BP_ALL	cysteine metabolic process	4	1.50E-03	Down
KEGG_PATHWAY	Cysteine metabolism	4	4.30E-02	Down
COG_ONTOLOGY	Cytoskeleton	9	6.40E-05	Up

Supplemental Data Table S9. Continued.

GOTERM_BP_ALL	cytoskeleton organization and biogenesis	43	1.70E-03	Up
GOTERM_BP_ALL	death	60	1.90E-02	Up
GOTERM_BP_ALL	developmental process	205	5.70E-05	Up
GOTERM_BP_ALL	dicarboxylic acid metabolic process	5	1.30E-03	Down
GOTERM_BP_ALL	DNA metabolic process	42	6.70E-03	Up
GOTERM_BP_ALL	DNA packaging	18	1.80E-02	Up
SP_PIR_KEYWORDS	dna recombination	4	2.00E-02	Up
GOTERM_BP_ALL	DNA replication	21	4.50E-04	Up
SP_PIR_KEYWORDS	dna replication	8	8.90E-03	Up
GOTERM_BP_ALL	DNA-dependent DNA replication	11	5.50E-03	Up
KEGG_PATHWAY	ECM-receptor interaction	15	2.00E-04	Up
GOTERM_BP_ALL	electron transport	31	1.70E-07	Down
COG_ONTOLOGY	Energy production and conversion	11	1.90E-04	Down
GOTERM_BP_ALL	establishment and/or maintenance of chromatin architecture	18	1.50E-02	Up
GOTERM_BP_ALL	establishment of cell polarity	4	2.40E-02	Up
GOTERM_BP_ALL	establishment of RNA localization	6	3.30E-02	Up
GOTERM_BP_ALL	fatty acid beta-oxidation	5	8.80E-03	Down
GOTERM_BP_ALL	fatty acid metabolic process	17	3.00E-04	Down
KEGG_PATHWAY	Fatty acid metabolism	7	1.30E-02	Down
SP_PIR_KEYWORDS	Fatty acid metabolism	7	4.00E-03	Down
GOTERM_BP_ALL	fatty acid oxidation	7	1.50E-03	Down
GOTERM_BP_ALL	flagellum biogenesis	3	1.20E-02	Down
GOTERM_BP_ALL	flagellum organization and biogenesis	3	1.80E-02	Down
KEGG_PATHWAY	Focal adhesion	27	6.40E-04	Up
GOTERM_BP_ALL	gene expression	156	6.30E-05	Up
GOTERM_BP_ALL	generation of precursor metabolites and energy	43	2.00E-09	Down
GOTERM_BP_ALL	gluconeogenesis	6	2.20E-03	Down
SP_PIR_KEYWORDS	gluconeogenesis	6	8.30E-05	Down
GOTERM_BP_ALL	glycerol metabolic process	3	4.00E-02	Down
GOTERM_BP_ALL	glycine metabolic process	3	4.90E-02	Down

Supplemental Data Table S9. Continued.

KEGG_PATHWAY	Glycine, serine and threonine metabolism	7	2.70E-03	Down
KEGG_PATHWAY	Glyoxylate and dicarboxylate metabolism	4	4.80E-03	Down
GOTERM_BP_ALL	growth	28	4.90E-02	Up
GOTERM_BP_ALL	hemopoietic or lymphoid organ development	19	4.50E-02	Up
GOTERM_BP_ALL	heterocycle metabolic process	11	1.20E-03	Down
GOTERM_BP_ALL	hexose biosynthetic process	6	4.20E-03	Down
KEGG_PATHWAY	Histidine metabolism	4	3.70E-02	Down
GOTERM_BP_ALL	humoral immune response mediated by circulating immunoglobulin	5	3.90E-02	Up
GOTERM_BP_ALL	I-kappaB kinase/NF-kappaB cascade	13	4.00E-02	Up
GOTERM_BP_ALL	immune response	38	1.10E-02	Up
SP_PIR_KEYWORDS	immune response	10	3.60E-02	Up
GOTERM_BP_ALL	immune system process	61	1.60E-04	Up
GOTERM_BP_ALL	intracellular protein transport	35	4.00E-02	Up
GOTERM_BP_ALL	intracellular transport	56	1.00E-02	Up
KEGG_PATHWAY	Leukocyte transendothelial migration	16	5.50E-03	Up
GOTERM_BP_ALL	lipid metabolic process	35	6.80E-04	Down
SP_PIR_KEYWORDS	lipid metabolism	9	8.00E-03	Down
GOTERM_BP_ALL	localization of cell	47	1.20E-05	Up
GOTERM_BP_ALL	L-serine metabolic process	3	4.00E-02	Down
GOTERM_BP_ALL	macromolecular complex assembly	44	8.70E-04	Up
GOTERM_BP_ALL	macromolecule biosynthetic process	78	4.60E-09	Up
GOTERM_BP_ALL	macromolecule localization	56	1.60E-02	Up
GOTERM_BP_ALL	macromolecule metabolic process	331	1.80E-08	Up
GOTERM_BP_ALL	male gamete generation	10	3.50E-02	Down
GOTERM_BP_ALL	metabolic process	391	5.60E-04	Up
GOTERM_BP_ALL	metabolic process	206	5.40E-05	Down
KEGG_PATHWAY	Metabolism of xenobiotics by cytochrome P450	14	2.60E-07	Down
GOTERM_BP_ALL	modification-dependent macromolecule catabolic process	16	8.30E-03	Up
GOTERM_BP_ALL	modification-dependent protein catabolic process	16	8.30E-03	Up

Supplemental Data Table S9. Continued.

GOTERM_BP_ALL	monocarboxylic acid metabolic process	30	7.20E-09	Down
GOTERM_BP_ALL	monosaccharide biosynthetic process	6	4.80E-03	Down
GOTERM_BP_ALL	mRNA metabolic process	18	5.00E-02	Up
SP_PIR_KEYWORDS	mrna processing	14	3.20E-03	Up
GOTERM_BP_ALL	mRNA processing	18	1.60E-02	Up
SP_PIR_KEYWORDS	mrna splicing	13	1.30E-03	Up
GOTERM_BP_ALL	mRNA transport	6	1.30E-02	Up
GOTERM_BP_ALL	multicellular organismal development	145	6.80E-03	Up
GOTERM_BP_ALL	muscle cell differentiation	9	2.60E-02	Up
GOTERM_BP_ALL	muscle fiber development	8	5.00E-02	Up
GOTERM_BP_ALL	negative regulation of apoptosis	26	1.20E-02	Up
GOTERM_BP_ALL	negative regulation of programmed cell death	27	7.00E-03	Up
GOTERM_BP_ALL	nitrogen compound biosynthetic process	11	2.50E-03	Down
GOTERM_BP_ALL	nitrogen compound catabolic process	13	2.60E-06	Down
GOTERM_BP_ALL	nitrogen compound metabolic process	41	3.30E-10	Down
GOTERM_BP_ALL	nonprotein amino acid metabolic process	3	2.50E-02	Down
GOTERM_BP_ALL	nuclear import	13	3.70E-03	Up
GOTERM_BP_ALL	nuclear transport	18	1.80E-03	Up
GOTERM_BP_ALL	nucleic acid transport	6	3.30E-02	Up
GOTERM_BP_ALL	nucleobase, nucleoside and nucleotide metabolic process	17	1.80E-03	Down
GOTERM_BP_ALL	nucleocytoplasmic transport	17	3.40E-03	Up
GOTERM_BP_ALL	nucleotide biosynthetic process	10	2.40E-02	Down
GOTERM_BP_ALL	nucleotide metabolic process	16	2.10E-03	Down
GOTERM_BP_ALL	organ development	96	7.90E-03	Up
GOTERM_BP_ALL	organelle organization and biogenesis	79	2.10E-04	Up
GOTERM_BP_ALL	organic acid metabolic process	59	2.90E-17	Down
GOTERM_BP_ALL	organic anion transport	4	1.90E-02	Down
GOTERM_BP_ALL	oxaloacetate metabolic process	3	3.90E-03	Down
KEGG_PATHWAY	Pentose and glucuronate interconversions	9	5.90E-07	Down
GOTERM_BP_ALL	peptide antigen transport	4	4.20E-02	Up

Supplemental Data Table S9. Continued.

GOTERM_BP_ALL	phosphate transport	9	2.60E-02	Up
KEGG_PATHWAY	Porphyrin and chlorophyll metabolism	10	2.00E-06	Down
GOTERM_BP_ALL	positive regulation of actin filament polymerization	4	6.80E-03	Up
GOTERM_BP_ALL	positive regulation of angiogenesis	6	1.10E-03	Up
GOTERM_BP_ALL	positive regulation of biological process	88	3.80E-03	Up
GOTERM_BP_ALL	positive regulation of cellular process	74	3.70E-02	Up
KEGG_PATHWAY	PPAR signaling pathway	8	4.50E-02	Down
GOTERM_BP_ALL	primary metabolic process	373	1.20E-06	Up
KEGG_PATHWAY	Propanoate metabolism	6	3.70E-03	Down
SP_PIR_KEYWORDS	protein biosynthesis	45	4.80E-16	Up
GOTERM_BP_ALL	protein catabolic process	18	4.50E-02	Up
SP_PIR_KEYWORDS	protein degradation	4	8.10E-03	Up
GOTERM_BP_ALL	protein import	12	3.20E-02	Up
GOTERM_BP_ALL	protein import into nucleus	12	8.40E-03	Up
GOTERM_BP_ALL	protein metabolic process	223	5.30E-09	Up
GOTERM_BP_ALL	protein polymerization	21	1.50E-11	Up
GOTERM_BP_ALL	protein transport	47	2.80E-02	Up
GOTERM_BP_ALL	protein-RNA complex assembly	15	4.20E-04	Up
GOTERM_BP_ALL	proteolysis	50	6.40E-03	Up
GOTERM_BP_ALL	proteolysis involved in cellular protein catabolic process	16	1.20E-02	Up
GOTERM_BP_ALL	pyrimidine nucleotide metabolic process	4	2.60E-02	Down
GOTERM_BP_ALL	pyrimidine ribonucleotide biosynthetic process	3	4.90E-02	Down
GOTERM_BP_ALL	pyruvate metabolic process	7	2.00E-03	Down
KEGG_PATHWAY	Pyruvate metabolism	9	3.70E-05	Down
KEGG_PATHWAY	Regulation of actin cytoskeleton	26	4.00E-03	Up
GOTERM_BP_ALL	regulation of actin cytoskeleton organization and biogenesis	13	9.00E-07	Up
GOTERM_BP_ALL	regulation of actin filament length	13	3.80E-07	Up
GOTERM_BP_ALL	regulation of actin filament polymerization	10	8.80E-08	Up
GOTERM_BP_ALL	regulation of actin polymerization and/or depolymerization	13	3.80E-07	Up
GOTERM_BP_ALL	regulation of biological process	220	1.80E-02	Up

Supplemental Data Table S9. Continued.

GOTERM_BP_ALL	regulation of cellular component organization and biogenesis	14	4.80E-04	Up
GOTERM_BP_ALL	regulation of cellular component size	13	5.90E-07	Up
GOTERM_BP_ALL	regulation of cellular process	192	2.00E-02	Up
GOTERM_BP_ALL	regulation of cytoskeleton organization and biogenesis	13	5.70E-06	Up
GOTERM_BP_ALL	regulation of organelle organization and biogenesis	13	5.70E-06	Up
GOTERM_BP_ALL	regulation of protein metabolic process	32	2.10E-04	Up
GOTERM_BP_ALL	regulation of translation	14	4.20E-02	Up
GOTERM_BP_ALL	response to biotic stimulus	20	3.90E-02	Up
GOTERM_BP_ALL	response to chemical stimulus	38	5.10E-03	Down
GOTERM_BP_ALL	response to external stimulus	59	2.40E-02	Up
GOTERM_BP_ALL	response to hormone stimulus	14	5.80E-03	Down
GOTERM_BP_ALL	response to nutrient	8	3.90E-02	Down
GOTERM_BP_ALL	response to organic substance	11	3.10E-02	Down
GOTERM_BP_ALL	response to other organism	13	3.70E-02	Up
GOTERM_BP_ALL	response to steroid hormone stimulus	9	3.50E-02	Down
GOTERM_BP_ALL	response to stimulus	143	5.00E-02	Up
GOTERM_BP_ALL	response to stress	86	7.80E-03	Up
GOTERM_BP_ALL	response to wounding	42	2.60E-02	Up
GOTERM_BP_ALL	response to xenobiotic stimulus	5	2.00E-02	Down
GOTERM_BP_ALL	ribonucleoprotein complex biogenesis and assembly	19	4.20E-04	Up
GOTERM_BP_ALL	ribonucleotide biosynthetic process	7	1.60E-02	Down
GOTERM_BP_ALL	ribonucleotide metabolic process	7	4.70E-02	Down
KEGG_PATHWAY	Ribosome	28	4.10E-11	Up
GOTERM_BP_ALL	RNA localization	6	3.90E-02	Up
GOTERM_BP_ALL	RNA processing	27	1.20E-02	Up
GOTERM_BP_ALL	RNA splicing	18	4.00E-03	Up
GOTERM_BP_ALL	RNA transport	6	3.30E-02	Up
GOTERM_BP_ALL	S-adenosylhomocysteine metabolic process	4	2.20E-02	Down
GOTERM_BP_ALL	serine family amino acid catabolic process	4	2.30E-03	Down
GOTERM_BP_ALL	serine family amino acid metabolic process	9	2.50E-06	Down

Supplemental Data Table S9. Continued.

GOTERM_BP_ALL	skeletal muscle fiber development	8	5.00E-02	Up
KEGG_PATHWAY	Small cell lung cancer	13	9.50E-03	Up
GOTERM_BP_ALL	sodium ion transport	8	5.00E-02	Down
SP_PIR_KEYWORDS	sodium transport	7	4.70E-02	Down
GOTERM_BP_ALL	spermatogenesis	10	3.50E-02	Down
KEGG_PATHWAY	Starch and sucrose metabolism	11	2.60E-06	Down
GOTERM_BP_ALL	sulfur amino acid catabolic process	3	1.80E-02	Down
GOTERM_BP_ALL	sulfur amino acid metabolic process	7	1.00E-04	Down
GOTERM_BP_ALL	sulfur compound biosynthetic process	5	1.60E-02	Down
GOTERM_BP_ALL	sulfur compound catabolic process	3	2.50E-02	Down
GOTERM_BP_ALL	sulfur metabolic process	14	2.10E-06	Down
SP_PIR_KEYWORDS	Symport	9	2.00E-03	Down
GOTERM_BP_ALL	system development	122	1.90E-02	Up
GOTERM_BP_ALL	tissue remodeling	18	3.20E-02	Up
KEGG_PATHWAY	Toll-like receptor signaling pathway	14	3.90E-03	Up
GOTERM_BP_ALL	transcription from RNA polymerase I promoter	4	2.40E-02	Up
GOTERM_BP_ALL	translation	68	7.30E-13	Up
GOTERM_BP_ALL	translational initiation	11	1.60E-03	Up
GOTERM_BP_ALL	tricarboxylic acid cycle	4	3.40E-02	Down
GOTERM_BP_ALL	tricarboxylic acid cycle intermediate metabolic process	5	4.30E-03	Down
KEGG_PATHWAY	Tryptophan metabolism	9	2.90E-04	Down
GOTERM_BP_ALL	ubiquitin-dependent protein catabolic process	16	7.60E-03	Up
SP_PIR_KEYWORDS	ubl conjugation	21	3.40E-02	Up
KEGG_PATHWAY	Valine, leucine and isoleucine degradation	9	1.60E-04	Down
GOTERM_BP_ALL	vitamin metabolic process	11	2.00E-04	Down
GOTERM_BP_ALL	water-soluble vitamin metabolic process	7	4.30E-03	Down
GOTERM_BP_ALL	wound healing	19	2.10E-02	Up
GOTERM_BP_ALL	xenobiotic metabolic process	5	1.80E-02	Down

LIST OF SYMBOLS, ABBREVIATIONS, AND ACRONYMS

ALT - alanine aminotransferase
ALKP - alkaline phosphatase
AMPB - amphotericin B
ANOVA – analysis of variance
AST - aspartate aminotransferase
BUN - urea nitrogen
CREA - creatinine
DAVID – database for annotation, visualization, and integrated discovery
DMT – Affymetrix data mining tool
DNA – deoxyribonucleic Acid
GenMAP – Gene MicroArray Pathway Profiler
HCA – hierarchical clustering of analysis
HE - hematoxylin and eosin
HPA - hippuric acid
KEGG – Kyoto encyclopedia of genes and genomes
MM - mismatch
NIAID - National Institute of Allergy and Infectious Diseases
PM – perfect match
PUR - puromycin
RNA – ribonucleic acid
SAM – significant analysis of microarrays
SOM – self organinzing map
TIBL - total bilirubin
TMeV - TIGR multiexperiment viewer
TP – total protein